

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 21:56:48 ; Search time 174 Seconds  
(without alignments)  
597,426 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 1058

Sequence: 1 MSEBIISVDRFLSLIEHH.....SSSSSSSSSENSGCRKKRY 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1058	100.0	203	2	Q9LDB6	Q9LDB6 catharanthu
2	382	36.1	210	2	Q9LEH6	Q9LEH6 catharanthu
3	358	33.8	226	2	Q8L9K1	Q8L9K1 arabidopsis
4	356.5	33.7	226	2	Q22167	Q22167 arabidopsis
5	356	33.6	202	2	Q8LBR3	Q8LBR3 glycine max
6	353	33.4	236	2	Q40476	Q40476 nicotiana t
7	345	32.6	282	2	Q9M4Y9	Q9M4Y9 mesembryant
8	339	32.0	237	2	Q9LW50	Q9LW50 nicotiana s
9	338	31.9	243	1	ERF2_ARATH	ERF2_ARATH
10	336	31.8	243	2	Q8LBU9	Q8LBU9 arabidopsis
11	333	31.5	233	2	Q40479	Q40479 nicotiana t
12	332.5	31.4	203	2	Q82447	Q82447 nicotiana t
13	330.5	31.2	244	2	Q84XB3	Q84XB3 lycopersico
14	328.5	31.0	234	2	Q04680	Q04680 lycopersico
15	324	30.6	268	1	ERF1_ARATH	ERF1_ARATH
16	323.5	30.6	235	2	Q9SE77	Q9SE77 matricaria
17	322.5	30.5	318	2	Q7XSD3	Q7XSD3 oryza sativ
18	322	30.4	328	2	Q7XU93	Q7XU93 oryza sativ
19	316.5	29.9	318	2	Q7XU94	Q7XU94 oryza sativ
20	306	28.9	303	2	Q949D4	Q949D4 oryza sativ
21	306	28.9	303	2	Q6H7H6	Q6H7H6 oryza sativ
22	296	28.0	201	2	Q84XB0	Q84XB0 lycopersico
23	296	28.0	345	2	Q949D2	Q949D2 oryza sativ
24	296	28.0	345	2	Q7XAD6	Q7XAD6 oryza sativ
25	292	27.6	344	2	Q6H6I3	Q6H6I3 oryza sativ
26	288	27.1	201	2	Q8LBD4	Q8LBD4 arabidopsis
27	286.5	27.1	244	2	Q9LND1	Q9LND1 arabidopsis
28	285.5	27.0	165	2	Q75UD5	Q75UD5 cucumis mel
29	285.5	27.0	201	2	Q9FKG2	Q9FKG2 arabidopsis
30	283.5	26.8	207	2	Q6V5B8	Q6V5B8 arabidopsis
31	282.5	26.7	207	2	Q6V5G9	Q6V5G9 arabidopsis

32	282.5	26.7	207	2	Q9LY05	Q9LY05 arabidopsis
33	282	26.7	206	2	Q6V5J8	Q6V5J8 brassica ol
34	281.5	26.6	207	2	Q6V5D3	Q6V5D3 olimariabido
35	277.5	26.2	218	2	Q6V5I2	Q6V5I2 sisymbrium
36	276.5	26.1	208	2	Q6WEP6	Q6WEP6 boechera dr
37	276	26.1	204	2	Q6V5F2	Q6V5F2 capsella ru
38	271.5	25.7	244	2	Q6Q4I4	Q6Q4I4 lycopersico
39	271	25.6	273	2	Q7X649	Q7X649 oryza sativ
40	271	25.6	273	2	Q9AQU3	Q9AQU3 oryza sativ
41	268	25.3	139	2	Q9LTC5	Q9LTC5 arabidopsis
42	268	25.3	198	2	Q6L4M2	Q6L4M2 oryza sativ
43	267.5	25.3	131	2	Q9L5X0	Q9L5X0 arabidopsis
44	266	25.1	161	1	PTIS LYCES	Q04681 lycopersico
45	265.5	25.1	268	2	Q9S2D6	Q9S2D6 arabidopsis

#### ALIGNMENTS

RESULT 1	ID	Q9LDB6	PRELIMINARY;	PRT;	203 AA.
AC	Q9LDB6				
DT	01-OCT-2000 (T-EMBLrel. 15, Created)				
DT	01-OCT-2000 (T-EMBLrel. 15, Last sequence update)				
DT	05-UTU-2004 (T-EMBLrel. 27, Last annotation update)				
DE	AP2-domain DNA-binding protein.				
GN	Name=orca3;				
OS	Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;				
OC	lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae;				
OC	Catharanthus.				
OX	NCBI_TaxID=4058;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPRAIN-G.don: TISSUE=Root;				
RX	MEDLINE=20355201; PubMed=10894776; DOI=10.1126/science.289.5477.295;				
RA	van der Fits L., Memelink J.;				
RT	"ORCA3, a jasmonate-responsive transcriptional regulator of plant				
RT	primary and secondary metabolism.";				
RL	Science 289:295-297(2000).				
DR	EMBL; AJ251250; CAB96900.1; -.				
DR	EMBL; AJ251249; CAB96899.1; -.				
DR	HSSP; O80337; ZGCC.				
DR	TRANSFAC; T04751; -.				
DR	GO; GO:0005634; C:nucleus; IEA.				
DR	GO; GO:0003700; P:transcription factor activity; IEA.				
DR	GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.				
DR	InterPro; IPR001471; TF_ERF.				
DR	PRINTS; PR00367; ETRHPELEMT.				
DR	Prodom; PD001423; TF_ERF.1.				
DR	SMART; SM00380; AP2; 1.				
KW	DNA-binding				
SO	SEQUENCE 203 AA; 22322 MW; CEE84C274312A601 CRC64;				
Query Match	100.0%;	Score 1058;	DB 2;	Length 203;	
Best Local Similarity	100.0%;	Pred. No. 3.4e-82;			
Matches	203;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSEBIISVDRFLSLIEHHLSLSDNDDSSSELTSTENWEEIFADFLNWSGSEIQKGS	60		
DB	1	MSEBIISVDRFLSLIEHHLSLSDNDDSSSELTSTENWEEIFADFLNWSGSEIQKGS	60		
QY	61	PSSESQCSNMAESCOEDSVVGTPEAAAGGCGSKDMNRYKGRAPMGFAAIEDPPK	120		
DB	61	PSSESQCSNMAESCOEDSVVGTPEAAAGGCGSKDMNRYKGRAPMGFAAIEDPPK	120		
QY	121	KSGRIWLTGYTEPEDAALAYDAAPFMGAKAKALNFPHLIGSNISGPVAVNPKRPPAEP	180		
DB	121	KSGRIWLTGYTEPEDAALAYDAAPFMGAKAKALNFPHLIGSNISGPVAVNPKRPPAEP	180		
QY	181	STTSSSSSSSENSGCRKKRY	203		

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Db      181 STTSSSSSSSSSSSGRKKRY 203
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RESULT 2
Q9LE66 PRELIMINARY; PRT; 210 AA.
AC Q9LE66;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AP2-domain DNA-binding protein.
GN Name=orca2;
OS Cathartacus roseus (Rose periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vincaceae;
OC Cathartacus.
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=G.don; TISSUE=Cell suspension;
RX MEDLINE=99380162; PubMed=10449411; DOI=10.1093/emboj/18.16.4455;
RA Menke F.L.H., Champion A., Kijne J.W., MemeLink J.;
RT "A novel jasmonate- and elicitor-responsive element in the periwinkle
RT secondary metabolite biosynthetic gene Ser interacts with a jasmonate-
RT and elicitor-inducible AP2-domain transcription factor, ORCA2.";
RL EMBL J.18.4455-4463(1999).
DR EMBL; AJ238740; CAB93940.1; -.
DR HSSP; O80337; ZGCC.
DR TRANSFAC; T04749; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR InterPro; IPR001471; TF_ERF.
DR PRINTS; PR00367; ETHRSPELEMT.
DR PRODOM; PD001423; TF_ERF.1.
DR SMART; SM00380; AP2; 1.
DR DNA-binding.
KW SEQUENCE 210 AA; 24021 MW; 017DF086F713CE38 CRC64;

Query Match 36.1%; Score 382; DB 2; Length 210;
Best Local Similarity 43.6%; Pred. No. 1.4e-24;
Matches 88; Conservative 27; Mismatches 35; Indels 52; Gaps 8;

QY 12 FLSLIEBHLISNSDSSSELTSTENBEIFADP-----LMSGSEIQKSGSPSSS 65
DB 14 FLEPLVDYOLFNNDFD-----FSEIFDFNVANNYNTSTSD-NFSGFQFMEN 60
QY 66 COS-----NSMAESC-----QEDSVVGTPEAAGAGGC----- 93
DB 61 CEETIEPNYASELSIIITLDFKODNYDEVAGQEELITPTSRGGGGGCEGRS 120
QY 94 SKDMNRYKGVRRRPMWKFPAEIRDPKKGSRIMLTGETPEPDALAYDAAMFMGAKAR 153
DB 121 NEEMWIRYGVRRRPMWKFPAEIRDPKKGSRIMLTGETPEPDALAYDAAMFMGAKAR 180
QY 154 LNFPHLIGNSISGPVAVNPRKR 175
DB 181 LNFPHLIGS-ANAPVAVSPRRR 201

RESULT 3
Q8L9K1 PRELIMINARY; PRT; 226 AA.
AC Q8L9K1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative ethylene response element binding protein (EREBP).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

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OC eutrosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY068387; AM65925.1; -.
DR HSSP; O80337; ZGCC.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR InterPro; IPR000977; DNA_Ligase.
DR PRINTS; PR00367; ETHRSPELEMT.
DR PRODOM; PD001423; TF_ERF.1.
DR SMART; SM00380; AP2; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
KW SEQUENCE 226 AA; 25367 MW; C3F80438CFE19D80 CRC64;

Query Match 33.8%; Score 358; DB 2; Length 226;
Best Local Similarity 44.8%; Pred. No. 1.7e-22;
Matches 79; Conservative 24; Mismatches 55; Indels 18; Gaps 5;

QY 21 LLSNDSSELTSTENBEIFADFLNWSGSEIQKSGSPSSSCQSNMAESCQEDSV 80
DB 26 ILNDNMSDLPUSDSDOD-----MAIYTLRAVASANTPSPVPTS-----PAEDK- 73
QY 81 VGTPEEAAAGGCS--KDMNRYKGVRRRPMWKFPAEIRDPKKGSRIMLTGETPEDAAL 138
DB 74 ---PPATKAGSHAPQKGQYGVRRRPMWKFPAEIRDPKKGARVIMLTGETPEDAAV 130
QY 139 AYDAAMFMGAKARLNFPHLIGNSISGPVAVNPRKRPAPETSSSSSSSEN 194
DB 131 AYDAAPQLGSRXAKLNFPHLIGSCXYEPVIRIRRRSP-EPVSQDLTSEQRGS 165

RESULT 4
Q22167 PRELIMINARY; PRT; 226 AA.
AC Q22167;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative ethylene response element binding protein (EREBP).
GN Name=Atg44840;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eutrosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
RA Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

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RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamuya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
 RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinzaki K.,  
 RA Ecker J., Theologis A., Davis R.W.,  
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,  
 RA Palm C.J., Theologis A., Ecker J., Davis R.W.,  
 RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,  
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamuya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
 RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinzaki K.,  
 RA Ecker J., Theologis A., Davis R.W.,  
 RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AC002388; AAC31840.1; -  
 DR EMBL: AF072471; AAL66886.1; -  
 DR EMBL: AF325089; AAK17157.1; -  
 DR EMBL: AF370540; AAK48967.1; -  
 DR PIR: T00409; T00409.  
 DR HSSP: 080337; 2GCC.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000977; DNA\_ligase.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS: PR00367; ETHRSPELEMT.  
 DR ProDom: PD001423; TF\_ERF; 1.  
 DR SMART: SM00380; AP2; 1.  
 DR PROSITE: PS00697; DNA\_LIGASE\_A1; UNKNOWN\_1.  
 SQ SEQUENCE 226 AA; 25353 MW; 4B2EF81CDD856987 CRC64;

Query Match 33.7%; Score 356.5; DB 2; Length 226;  
 Best Local Similarity 61.1%; Pred. No. 2.3e-22;  
 Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;

QY 84 PPEAAAGGCGS--KDMRYKGVRRPMPGKFAEIRDPKKGSRIMLTETPEDAALAYD 141  
 DB 74 PPRTRKSSGSHAPQKMGQRRGVRRRPMPGKFAEIRDPKKGARAWLCTYTPEDAAVAYD 133  
 QY 142 AAFAFNMGAKARLNPFLIGSNISGPRVNPFRKRFPAEPSTSSSSSSSEN 194  
 DB 134 RAAFGRRGSKAKLNPFLIGSCKEPVRIRPRRSP-EPSPVQDLTSEQKRES 165

RESULT 5  
 Q08LR3 PRELIMINARY; PRT; 202 AA.  
 AC 08LR3;  
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Ethylene-responsive element binding protein 1.  
 GN Name=EREBP1;  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 NCBI\_TaxID=3847;  
 RX MEDLINE=22054140; PubMed=12059106;  
 RA Mazarei M., Puhoff D.P., Hart J.K., Rodermeil S.R., Baum T.J.;  
 RT "Identification and characterization of a soybean ethylene-responsive  
 RT element binding protein gene whose mRNA expression changes during  
 RT soybean cyst nematode infection.";  
 RL Mol. Plant Microbe Interact. 15:577-586 (2002).  
 DR EMBL: AF357211; AAM45475.1; -

DR HSSP: 080337; 2GCC.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000977; DNA\_ligase.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS: PR00367; ETHRSPELEMT.  
 DR ProDom: PD001423; TF\_ERF; 1.  
 DR SMART: SM00380; AP2; 1.  
 DR PROSITE: PS00697; DNA\_LIGASE\_A1; UNKNOWN\_1.  
 SQ SEQUENCE 202 AA; 22467 MW; 1B875A6EB2A7D56D CRC64;

Query Match 33.6%; Score 356; DB 2; Length 202;  
 Best Local Similarity 41.3%; Pred. No. 2.2e-22;  
 Matches 83; Conservative 29; Mismatches 55; Indels 34; Gaps 5;

QY 9 SDRFLLSLIEHLISDSDSSSELTSTENMEIFADFLNMSGSEIQKRGSSSSCGS 68  
 DB 8 SDFAPLESVQVYLLGHDSTINLMSETHQAASH--DPESD-----PNKCDGDS 51  
 QY 69 NSMAESCCQEDSVY----GTPPEAAAGGCGSKDMRYKGVRRPMPGKFAEIRDPKKGSR 124  
 DB 52 GNIAFRSEBDATAVVADHAP-----TWKHYRGVRRPMPGKFAEIRDPKKGAR 101  
 QY 125 IMLTETPEDAALAYDAAAFNMGAKARLNPFLIGSN----ISGPRVNPFRKRFPAEP 180  
 DB 102 VMIGTYDTEKALADKAAFKRGOKAKLNPFLIGSDLSSEFVMMTTSKSLLEI 161  
 QY 181 STTSSSSSSSSSENSGKRKR 201  
 DB 162 SSPSSSCSDSSSSSQGTGKRK 182

RESULT 6  
 Q04076 PRELIMINARY; PRT; 236 AA.  
 ID Q04076;  
 AC Q04076;  
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE ERF1.  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BY4; TISSUE=leaf;  
 RX MEDLINE=95276459; PubMed=7756828;  
 RA Ohme-Takagi M., Shinshi H.,  
 RT "Ethylene-inducible DNA binding proteins that interact with an  
 RT ethylene responsive element.";  
 RL Plant Cell 7:173-182 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BY4; TISSUE=Leaf;  
 RA Suzuki K., Suzuki N., Ohme-Takagi M., Shinshi H.;  
 RT "Immediate early induction of mRNAs for ethylene-responsive  
 RT transcription factors in tobacco leaf strips after cutting.";  
 RL Plant J 15:657-665 (1998).  
 DR EMBL: D38123; BAA07321.1; -  
 DR PIR: T02432; T02432.  
 DR HSSP: 080337; 2GCC.  
 DR TRANSFAC: T02653; -  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS: PR00367; ETHRSPELEMT.  
 DR ProDom: PD001423; TF\_ERF; 1.  
 DR SMART: SM00380; AP2; 1.  
 SQ SEQUENCE 236 AA; 26520 MW; 6B030DEB9BFEDE2D5 CRC64;

Query Match 33.4%; Score 353; DB 2; Length 236;  
 Best Local Similarity 45.3%; Pred. No. 4.9e-22;  
 Matches 81; Conservative 20; Mismatches 50; Indels 28; Gaps 6;

QY 27 DSSSLSTTEENWEIIFADFLN--WSSEIQKRGSPSESCQSNMAESCOEDSVVTP 84  
 DB 46 DSEDMWIVYT-----LKDALNVGMSPPNF-SAGEVXSEQ-----REEIVVSP 88  
 QY 85 PEAAGCGCKDMNR-YKGVRRPVGKFAEIRDPKKGSRIWLTGYETPEDALAYDAA 143  
 DB 89 AETTAAPAELEPRGRHYRVRPCKGFAEIRDPKKNARVWLGTETDEDAIAYDKA 148  
 QY 144 AFNRGAKARLNPPLHIGSNISGPRVNPVKRFPAPSTSSSSSSSSSSSGKRRK 202  
 DB 149 AYMRGSKALNLPFHRIGLNEPEPVVTAKRASPEP-----ASSSENSPRRRK 199

## RESULT 7

Q9M4Y9 PRELIMINARY; PRT; 282 AA.  
 AC Q9M4Y9;  
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE AP2-related transcription factor (Ethylene responsive protein).  
 GN Name=CDBP; Synonyms=EREB;  
 OS Mesembryanthemum crystallinum (Common ice plant).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Alzooceae; Mesembryanthemum.  
 NCBI\_TaxID=3544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA Scharte J., Baur B.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hou Y.-X., Cheng X.-G., Zhang J.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP245119; AAP63205.1; -;  
 DR EMBL; AE37265; AAP80810.1; -;  
 DR HSSP; 080337; 2GCC.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR PRINTS; PRO0367; ETRHSPLEMMT.  
 DR ProDom; PD001423; TF\_ERF.1.  
 DR SMART; SM00380; AP2\_1.  
 SQ SEQUENCE 282 AA; 30011 MW; 617C32009C535B29 CRC64;

Query Match 32.6%; Score 345; DB 2; Length 282;

Best Local Similarity 40.5%; Pred. No. 2.9e-21;  
 Matches 96; Conservative 22; Mismatches 63; Indels 56; Gaps 10;

QY 9 SDRFLSLTEHLLSD-----NSDDSS-----SELSTSTEEN 39  
 DB 9 SDRAVLESTIRKHLLEWDPAGAPATTTGSGPYRHNSFSLYPLCLTNWGBLPKEDD 68  
 QY 40 WEERF-----ADFLNM--SGSEIQKRGSPSESCQSNMAESCOEDSVVTP-PEAA 88  
 DB 69 SEDMWVFGVLRDAVHTGMSQSGSE-SGSGSPAPVTVKPEPV-----DSPVSSAPRV 121  
 QY 89 AGC-----GCKDMNRKYGVRRPVGKFAEIRDPKKGSRIWLTGYETPEDALAYDAA 143  
 DB 122 AGCEAVVAAPARCKYRGVRRPVGKFAEIRDPKKNARVWLGTETDEDAIAYDKA 181  
 QY 144 AFNRGAKARLNPPLHIGSNISGPRVNPVKRFPAPSTSSSSSSSSSSSGKRRK 200  
 DB 182 AFMRGSKALNLPFHRIGLNEPEPVVTAKRASPEP-----ASSSENSPRRRK 234

## RESULT 8

Q9LW50 PRELIMINARY; PRT; 237 AA.

AC Q9LW50;  
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Ethylene-responsive element binding factor.  
 GN Name=erf2;  
 OS Nicotiana glauca (Wood tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 NCBI\_TaxID=4096;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=20399450; PubMed=10945353;  
 RA Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;  
 RT "Characterization of gene expression of NERFs, transcription factors  
 of basic PR genes from Nicotiana glauca."  
 RL Plant Cell Physiol. 41:817-824(2000).  
 DR EMBL; AB016264; BAA97122.1; -;  
 DR HSSP; 080337; 2GCC.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR PRINTS; PRO0367; ETRHSPLEMMT.  
 DR ProDom; PD001423; TF\_ERF.1.  
 DR SMART; SM00380; AP2\_1.  
 SQ SEQUENCE 237 AA; 26243 MW; 01BC3EBE51E46298 CRC64;

Query Match 32.0%; Score 339; DB 2; Length 237;

Best Local Similarity 44.3%; Pred. No. 7.7e-21;  
 Matches 82; Conservative 23; Mismatches 54; Indels 26; Gaps 7;

QY 24 DNSDDSS-----SSELTSTEENWEIIFADFLNWSGSEIQKRGSPSESCQSNMAESCOE 77  
 DB 37 DSEDMWIVYGLSDALYT--GWTP-----FNLTSTEI--KAPFREIEPATSPVPS--- 83  
 QY 78 DSVYGTPEEAAAGCGCKDMNRKYGVRRPVGKFAEIRDPKKGSRIWLTGYETPEDA 137  
 DB 84 ---VAPEAETTTAAVVPKGRHYRVRPCKGFAEIRDPKKNARVWLGTETDEDA 140  
 QY 138 LAYDAAFNRGAKARLNPPLHIGSNISGPRVNPVKRFPAPSTSSSSSSSSSSSGKRRK 197  
 DB 141 LAYDKAAYMRGSKALNLPFHRIGLNEPEPVVTAKRASPEP-----ASSISPAISNSLP 196  
 QY 198 RKKRR 202  
 DB 197 KRRRK 201

## RESULT 9

EF2\_ARATH STANDARD; PRT; 243 AA.

AC Q9LW50;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ethylene responsive element binding factor 2 (AtERF2).  
 GN Name=ERF2; Synonyms=ERF-2; OrderedLocustNames=At5g47220;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=20181733; PubMed=10715325;  
 RA Fujimoto S.Y., Ohta M., Ueul A., Shinshi H., Ohme-Takagi M.;



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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OK NCBI_TaxID=3702;
RN
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovsky N., Town C.D., Troughan M., Alexandrov N.,
RA Feldmann K.A., Flavel R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
annotation."
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavel R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR HSSP; AY086983; AAM4544.1; -.
DR HSSP; O80337; 2GCC.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001471; TF_ERF.
DR PRINTS; PR00367; ETHRSPLEMT.
DR ProDom; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
SQ SEQUENCE 243 AA; 26728 MW; A2DA6978560CB490 CRC64;
DQ
Query Match 31.8%; Score 336; DB 2; Length 243;
Best Local Similarity 39.4%; Pred. No. 1.4e-20;
Matches 85; Conservative 29; Mismatches 70; Indels 32; Gaps 6
QY 9 SDRFLSLIEBHLSDSDSSSELTSTENWEEIFADFLNWSSEIQKRS----- 60
DB 9 SDVALLSITRHLGGGGE---NLRNLNESPSSCFTE--SWGGLPKENDEMLVYGL 63
QY 61 -PSESCQSNMAESCCED-----SVGVTPPEAAGGCSKDMRYKGVRR 106
DB 64 LKDFHFDTSDDISCFDPFAVAVTEPTENFTAMEEKPKAIPTETAVKAKHYGVRR 123
QY 107 PMGFAAEIHPDKKGRIMVGTETPEDALAYDAAPNMRGAKARLNPHLIGSNISG 166
DB 124 PMGFAAEIRPAPANGARVWLGTEIYEDDALAYDIAPFRKSSSALLNPLRVNSGEPD 183
QY 167 PVRVNPKRFPAPBPTTSSSSSSSSSSSGGRKKR 202
DB 184 PVRITSKR---SSSSSSSSSSSTSSSEN--GKLKR 214
RESULT 11
Q040479 PRELIMINARY; PRT; 233 AA.
ID 040479;
AC 040479;
RT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Ethylene-responsive element binding protein.
GN Name=EREBP-2;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC lamids; Solanales; Solanaceae; Nicotiana.
OC NCBI_TaxID=4097;
RN
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BY4; TISSUE=Leaf;
RX MEDLINE=95276459; PubMed=7756828;
RA Ohme-Takagi M., Shimizu H.;
RT "Ethylene-inducible DNA binding proteins that interact with an
RT ethylene responsive element."
RL Plant Cell 7:1173-182 (1995).
RN
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN-BY4; TISSUE=Leaf;  
 RA Suzuki K., Suzuki N., Ohme-Takagi M., Shinshi H.;  
 RT "Immediate early induction of mRNA for ethylene-responsive  
 transcription factors in tobacco leaf strips after cutting."  
 RL Plant J. 15:657-665(1998).  
 DR EMBL; D8126; BAA07324.1; -.  
 DR PIR; T02590; T02590.  
 DR HSSP; O80337; 2GCC.  
 DR TRANSFAC; T02654; -.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETHRSPLEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SQ SEQUENCE 233 AA; 25563 MW; 6CD16783582CC0B5 CRC64;

Query Match 31.5%; Score 333; DB 2; Length 233;  
 Best Local Similarity 54.9%; Pred. No. 2.4e-20;  
 Matches 67; Conservative 16; Mismatches 35; Indels 4; Gaps 2;

QY 81 VCTPPPAAGGCGCKDMNRKYGVRRPMPCKFAAEIRDPKKGSRIWLGTYETPEDALAY 140  
 DB 80 VAPPAETTAQAVVPKGRHYGVRRPMPCKFAAEIRDPKNGARVWLGTETAEBAALAY 139  
 QY 141 DAAAFMRGAKARLNPFLIGSNISGPVVRNPKRPPAEPSTSSSSSSSSSSSGGRKK 200  
 DB 140 DKAAVMRSGKALNPFHRIGLNEPEPVATKRRSP-EP---ASSSSISALENSGPKRR 195

QY 201 RR 202  
 DB 196 RK 197

RESULT 12  
 ID 082447 PRELIMINARY; PRT; 203 AA.  
 AC 082447;  
 DT 01-NOV-1998 (T-EMBLrel. 08, Created)  
 DT 01-NOV-1998 (T-EMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Ethylene response element binding protein 1 (Fragment).  
 GN Name=EREBP1;  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 OC NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98392433; PubMed=9725022;  
 RA Horvath D.M., Huang D.J., Chua N.H.;  
 RT "Four classes of salicylate-induced tobacco genes."  
 RL Mol. Plant Microbe Interact. 11:895-905(1998).  
 DR EMBL; AF057373; AAC62619.1; -.  
 DR HSSP; O80337; 2GCC.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETHRSPLEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 FT NON TER 1  
 SQ SEQUENCE 203 AA; 22616 MW; F62AB477B0B017DE CRC64;

Query Match 31.4%; Score 332.5; DB 2; Length 203;  
 Best Local Similarity 41.8%; Pred. No. 2.3e-20;  
 Matches 77; Conservative 20; Mismatches 50; Indels 37; Gaps 6;

QY 37 EENWEE-----IFADPLN--WSGSEIQKRGSPSSSCQNSMAESCQDS 79  
 AC 37 EENWEE-----IFADPLN--WSGSEIQKRGSPSSSCQNSMAESCQDS 79

DB 2 EETWGBLPLKVDSEDMVIYTLIKDALNVGWSGFNF-TAGEVYKSE-----LMEEB 50  
 QY 80 VCTPPPAAGGCGCKDMNR- YKGVRRPMPCKFAAEIRDPKKGSRIWLGTYETPEDAL 138  
 DB 51 IVVSPADTTAPPAELPRGRHYGVRRPMPCKFAAEIRDPKNGARVWHRITETDEAAI 110  
 QY 139 AYDAAAFMRGAKARLNPFLIGSNISGPVVRNPKRPPAEPSTSSSSSSSSSSSGGR 198  
 DB 111 AYDKAAVMRSGKALNPFHRIGLNEPEPVATKRRASPEP-----ASSSENSAK 162  
 QY 199 KRR 202  
 DB 163 RRRK 166

RESULT 13  
 ID 084XB3 PRELIMINARY; PRT; 244 AA.  
 AC 084XB3;  
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Ethylene response factor 1.  
 GN Name=ERF1;  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 OC NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22816770; PubMed=12935902; DOI=10.1016/S0014-5793(03)00757-9;  
 RA Tournier B., Sanchez-Ballester M.T., Jones B., Peesquet E., Regad F.,  
 RA Latche A., Pech J.C., Bouzaïen M.;  
 RT "New members of the tomato ERF family show specific expression pattern  
 and diverse DNA-binding capacity to the GCC box element."  
 RL FEBS Lett. 550:149-154(2003).  
 DR EMBL; AY192367; AAC034703.1; -.  
 DR HSSP; O80337; 2GCC.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETHRSPLEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SQ SEQUENCE 244 AA; 27085 MW; D090818A6CE5B833 CRC64;

Query Match 31.2%; Score 330.5; DB 2; Length 244;  
 Best Local Similarity 39.2%; Pred. No. 4.2e-20;  
 Matches 78; Conservative 21; Mismatches 61; Indels 39; Gaps 4;

QY 26 SDDSSSELTSTERNW-----EIRADPL-----NWSGSEIQKRGSPSS 63  
 DB 23 SSSFSSTLMPCLTBSWGDLPKVDSEDMVIYGLQDAFSGWTPSNLTSEVVLBPREEI 82  
 QY 64 SSCOSNMASSCQDVSVGTPEPAAGGCGCKDMNRKYGVRRPMPCKFAAEIRDPKKGS 123  
 DB 83 EPMSTSVS-----PPTVAPALAQPKGRHYGVRRPMPCKFAAEIRDPKNGA 130  
 QY 124 RIMWLGTYETPEDALAYDAAAFMRGAKARLNPFLIGSNISGPVVRNPKRPPAEPSTT 183  
 DB 131 RVMWLGTYESAEBEALAYGKAFAFMRGKALNPFHRIGLNEPEPVATVGRRL-----SE 185  
 QY 184 SSSSSSSSSSSSGRKKRR 202  
 DB 186 SASSSVSSASGSGSPKRR 204

RESULT 14  
 ID 004680 PRELIMINARY; PRT; 234 AA.  
 AC 004680;  
 DB 004680;

DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Pe14 (Fragment).  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 NC NCB1\_TaxID=4081;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97357308; PubMed=9214637; DOI=10.1093/emboj/16.11.3207;  
 RA Zhou J., Tang X., Martin G.B.;  
 RT "The Pto kinase conferring resistance to tomato bacterial speck  
 disease interacts with proteins that bind a cis-element of  
 pathogenesis-related genes."  
 RT EMBO J. 16:3207-3218 (1997).  
 RL (2)  
 RN SEQUENCE FROM N.A.  
 RA Zhou J., Tang X., Martin G.B.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U89255; AAC50047.1; -  
 DR PIR; T07686; T07686.  
 DR HSSP; O80337; 2GCC.  
 DR TRANSFAC; T04715; -  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR INTERP; IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETRSPPELEMT.  
 DR Prodom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 FT NON\_TER 234 234  
 SQ SEQUENCE 234 AA; 26001 MW; FC96F5690F08AAA4A CRC64;  
 QY Best Match 31.0%; Score 328.5; DB 2; Length 234;  
 QY Query local similarity 47.1%; Pred. No. 5.9e-20;  
 Matches 73; Conservative 18; Mismatches 43; Indels 21; Gaps 5;  
 QY 49 NMSGSEIQRKSPSSSCSNMAESCOEDSVVGTPEEAAAGGCSKDMNR-YKGVRRP 107  
 65 NFFAGGV--KSEPRE-----IESSPES--PSPAFETAAAPAEPRKGRHVRGRQR 113  
 DB 108 WGFPAEIDPKKKKGRIMVGTETPEDAALAYDAANFNKAKARINPFLIGSNISGP 167  
 114 WGFPAEIRDPKNGKRWVLTETPEEAAIADKAAVRRMSKAKHLNPHRIGLNEPEP 173  
 QY 168 VRVNPKRFPAPSPSTSSSSSSSSSSSGRKKRR 202  
 DB 174 VRVTAKRKRAPSP-----ASSSGNGSKRRR 199  
 RESULT 15  
 ERFL\_ARATH STANDARD; PRT; 268 AA.  
 AC 080337; Q93236; Q9SUK1;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ethylene responsive element binding factor 1 (AtERF1) (ERESP-2  
 protein).  
 GN Name:ERF1; Synonyms=ERF-1; OrderedLocusNames=At4g17500;  
 GN ORFNames=D14785W;  
 GN Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 NC NCB1\_TaxID=5702;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Chen E., Maria M.A., Marijansen R., McCombie W.R.;  
 RX MEDLINE=20181733; PubMed=10715325;  
 RA Fujimoto S.Y., Ohta M., Usui A., Shinnhi H., Ohme-Takagi M.;

RT "Arabidopsis ethylene responsive element binding factors act as  
 RT transcriptional activators or repressors of GCC box mediated gene  
 RT expression.";  
 RT Plant Cell 12:393-404 (2000).  
 RL (2)  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=98121113; PubMed=9461215; DOI=10.1038/35140;  
 RA Bevan M., Bancroft I., Bent E., Love K., Goodman H.M., Dean C.,  
 RA Bergkamp R., Dirks W., van Staveren W., Stiekema W., Drost L.,  
 RA Ridley P., Hudson S.-A., Patel K., Murphy G., Piffanelli P.,  
 RA Wedler H., Wedler E., Wambutt R., Weitzengesser T., Pohl T., Terry N.,  
 RA Gielen J., Villarroel R., De Clercq R., van Montagu M., Lecharny A.,  
 RA Aubourg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S.,  
 RA Kotter P., Entian K.-D., Rieger M., Schaefer M., Funk B.,  
 RA Mueller-Auer S., Silvey M., James R., Montfort A., Pons A.,  
 RA Pivdomech P., Douka A., Vouklatou E., Milioni D., Hatzopoulos P.,  
 RA Pivdomech E., Obermaier B., Hilbert H., Duesterhoeft A., Moores T.,  
 RA Jones J.D.G., Eneva T., Palme K., Benes V., Reichmann S., Ansgore W.,  
 RA Cooke R., Berger C., Delseny M., Voet M., Volckaert G., Mewes H.-W.,  
 RA Kosterseman S., Schueller C., Chalwatzis N.;  
 RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of  
 RT Arabidopsis thaliana.";  
 RL Nature 391:485-486 (1998).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;  
 RA Moyer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,  
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,  
 RA Harris B., Ansgore W., Brandt P., Grivell L.A., Rieger M.,  
 RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,  
 RA Kreis M., Delseny M., Pivdomech P., Watson M., Schmidtheim T.,  
 RA Reichert B., Portetlelle D., Perez-Alonso M., Boutry M., Bancroft I.,  
 RA Vos P., Hohenseil J., Zimmermann W., Wedler H., Ridley P.,  
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,  
 RA van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,  
 RA Braeken M., Weljens I., Voet M., Bastiaens I., Aert R., Defoor E.,  
 RA Weitzengesser T., Bothe G., Rampsperger U., Hilbert H., Braun M.,  
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirks W.,  
 RA Moolman P., Klein lankhorst R., Rose M., Hauf J., Koetter P.,  
 RA Bernieris S., Hempel S., Feldpausch M., Lambirth S., Van den Daele H.,  
 RA de Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,  
 RA van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,  
 RA Clark L., Doggett J., Hall S., Kay W., Lennard N., Mcley K., Mayes R.,  
 RA Pectict A., Rajadream M.A., Lyne M., Benes V., Reichmann S.,  
 RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehert T.-H.,  
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzi A.,  
 RA Neumann S., Argitrou A., Vitale D., Liguori R., Pivandri E.,  
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,  
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,  
 RA Cheffor F., Cooke R., Berger C., Montfort A., Casacuberta E.,  
 RA Gibbons T., Weber N., Vandenbol M., Bagnies M., Terol J., Torres A.,  
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,  
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bieleke C.,  
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,  
 RA Zaccaria P., Bevan M., Wilson R.K., de la Baetie M., Habermann K.,  
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Siegel L.,  
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,  
 RA Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,  
 RA Latreille P., Courtney L., Cloud U., Abbott A., Scott K., Johnson D.,  
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,  
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,  
 RA Nelson J., Splich J., Ryan E., Andrews S., Giesel C., Layman D.,  
 RA Du H., Ali J., Berghoff A., Jones K., Drono K., Cotton M., Joshi C.,  
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,  
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,  
 RA Swaby I.K., O'Shaughnessy A., Rodriguez W., Hoffman U., Tili S.,  
 RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodi M., Johnson A.,  
 RA Chen E., Maria M.A., Marijansen R., McCombie W.R.;  
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
 RT thaliana.";

RL Nature 402:769-777(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;  
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.U.,  
 RA Karlthick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,  
 RA Karlin-Nemman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,  
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,  
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,  
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,  
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
 RA Satou M., Tamse R., Vayenberg M., Wallender E.K., Wong C., Yamamura Y.,  
 RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.,  
 RT "Empirical analysis of transcriptional activity in the Arabidopsis  
 RT genome.";  
 RL Science 302:842-846(2003).  
 RN [5]  
 RP STRUCTURE BY NMR OF 146-208.  
 RX MEDLINE=98409552; PubMed=973626; DOI=10.1093/emboj/17.18.5484;  
 RA Allen M.D., Yamasaki K., Ohme-Takagi M., Tateo M., Suzuki M.,  
 RT "A novel mode of DNA recognition by a beta-sheet revealed by the  
 RT solution structure of the GCC-box binding domain in complex with  
 RT DNA.";  
 RL EMBO J. 17:5484-5496(1998).  
 RN [6]  
 RP INDUCTION.  
 RX MEDLINE=99069218; PubMed=9851977;  
 RA Solano R., Stepanova A.N., Chao Q., Ecker J.R.,  
 RT "Nuclear events in ethylene signaling: a transcriptional cascade  
 RT mediated by ETHYLENE-INSENSITIVE3 and ETHYLENE-RESPONSE-FACTOR1.";  
 RL Gene Dev. 12:3703-3714(1998).  
 CC -1- FUNCTION: transcription factor that binds to the GCC-box  
 CC pathogenesis-related promoter element.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- INDUCTION: Ethylene induction of ERF1 is completely dependent on a  
 CC functional ETHYLENE-INSENSITIVE3 (EIN3) protein.  
 CC -1- SIMILARITY: Contains 1 AP2/ERF domain.  
 CC -1- CAUTION: Ref.2 and Ref.3 sequences differ from that shown due to a  
 CC frameshift in position 44.  
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-3 is the initiator.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL; AB008103; BAB32418.1; ALT\_INIT.  
 DR EMBL; Z97343; CAB45963.1; ALT\_FRAME.  
 DR EMBL; AL161546; CAB78753.1; ALT\_FRAME.  
 DR EMBL; AY058174; AAL25588.1;  
 DR EMBL; AY062533; AAL32611.1;  
 DR EMBL; BT002578; AAC00938.1;  
 DR PDB; 1GCC; NMR; A=144-206.  
 DR PDB; 2GCC; NMR; @=141-210.  
 DR PDB; 3GCC; NMR; @=141-210.  
 DR TRANSFAC; T04633;  
 DR InterPro; IPR001471; TF\_ERF.  
 DR Pfam; PF00847; AP2\_1.  
 DR PRINTS; PR00367; ETRSPLELMT.  
 DR ProDom; PD001423; TF\_ERF\_1.  
 KM 3D-structure; DNA-binding; Nuclear protein; Transcription regulation.  
 FT DNA BIND 143 208 AP2/ERF.  
 SQ SEQUENCE 268 AA; 29189 MW; 0FB7839984E97B50 CRC64;

Query Match 30.6%; Score 324; DB 1; Length 268;  
 Best Local Similarity 36.0%; Pred. No. 1.7e-19;

Matches	91; Conservative	27; Mismatches	69; Indels	66; Gaps	9;
Oy	1 MSEELISVSDRFLSLIEEHLSDN---- <td></td> <td></td> <td></td> <td>36</td>				36
Db	1 MSMTADSQSYATLLESIRRLLESEBRIILSESTASSVTQSCVTCGQIKPYGNPFSKL 60				
Oy	37 ----EENW-----EELFADFL-----NW-----SGSEIQKRGSPS--SESCQSN 69				
Db	61 YPCPTESWMDLPKLENDSEMDLVYGLINDAFHCGWEPSSSSSDSDRSSFPVXIEPTESF 120				
Oy	70 SMAESCQEDSVGTTPPAAAGGCGSKDMRYKGVRRBPPCKFAELRDPKKGRIMLGT 129				
Db	121 AAVDSVVKKEKTSVSAAYTAAGK--HYRGVROPWCKFAELRDPAKNGARVWLGT 177				
Oy	130 YETPEDAALAYDAAFVNRGAKARLNPPLIGSNIISGPVYVNPKRFPAPSTSSSSSS 189				
Db	178 FETIEDAALAYDRAAFMRGRSLINFLPLRVNGGEFDPVRIKSR-----SST 226				
Oy	190 SSENSSGGRKKR 202				
Db	227 SSNEN-GAPKKR 238				

Search completed: February 27, 2005, 22:06:06  
 Job time : 177 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 21:48:28 ; Search time 163 Seconds

(without alignments)  
481.671 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 1058  
Sequence: 1 MSEELISVSDRFLSLIEH.....SSSSSSSSSGRGRKKRRY 203

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq.16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1058	100.0	203	3	AA97228	Aay97228 Plant tra
2	400	37.8	227	8	ADG00355	Adg00355 Nicotiana
3	382	36.1	210	3	AA97227	Aay97227 Plant tra
4	358	33.8	212	3	AAG24800	Aag24800 Arabidops
5	358	33.8	226	3	AAG24799	Aag24799 Arabidops
6	357.5	33.8	183	3	AAG24801	Aag24801 Arabidops
7	356.5	33.7	183	3	AAG34782	Aag34782 Arabidops
8	356.5	33.7	212	3	AAG34781	Aag34781 Arabidops
9	356.5	33.7	226	4	AAB02464	Aae02464 Arabidops
10	356.5	33.7	226	4	AAB02464	Aae02464 Arabidops
11	356.5	33.7	226	7	AD337189	Ad337189 Plant yie
12	356.5	33.7	226	8	AD141543	Ad141543 Plant tra
13	356.5	33.7	226	8	AD001615	Ad001615 Thalecres
14	356.5	33.7	226	8	ADN73807	Adn73807 Thalecres
15	356	33.6	202	8	ADM72373	Adm72373 Soybean N
16	356	33.6	202	8	ADM72375	Adm72375 Soybean N
17	348	32.6	282	8	AD142040	Ad142040 Plant tra
18	348	31.9	243	4	AAE02522	Aae02522 Arabidops
19	338	31.9	243	5	AA093144	Aa093144 Arabidops
20	338	31.9	243	7	AB043109	Ab043109 A. thalia
21	338	31.9	243	8	AD143611	Ad143611 Plant tra
22	338	31.9	243	8	AD002257	Ad002257 Thalecres
23	338	31.9	243	8	AD003419	Ad003419 Thalecres
24	338	31.9	244	3	AAG43672	Aag43672 Arabidops
25	336	31.8	243	3	AA08167	Aa08167 Arabidops

26	324	30.6	268	3	AA05106	Aa05106 Arabidops
27	324	30.6	268	4	AAE02506	Aae02506 Arabidops
28	324	30.6	268	5	AAU92963	Aau92963 Arabidops
29	324	30.6	268	6	ADB23098	Adb23098 Environme
30	324	30.6	268	7	AB043101	Ab043101 A. thalia
31	324	30.6	268	7	AD337257	Ad337257 Plant yie
32	324	30.6	268	8	AD141547	Ad141547 Plant tra
33	324	30.6	268	8	AD001625	Ad001625 Thalecres
34	322	30.4	266	3	AA05107	Aa05107 Arabidops
35	321.5	30.4	266	3	AA03674	Aa03674 Arabidops
36	321.5	30.4	187	3	AA03673	Aa03673 Arabidops
37	319.5	30.2	147	3	AA08169	Aa08169 Arabidops
38	319.5	30.2	186	3	AA08168	Aa08168 Arabidops
39	316	29.9	250	3	AA045283	Aa045283 Arabidops
40	312	29.5	188	3	AA05108	Aa05108 Arabidops
41	312	29.5	188	3	AA045284	Aa045284 Arabidops
42	312	29.5	188	3	AA043437	Aa043437 Arabidops
43	312	29.5	188	8	ADN72841	Adn72841 Thalecres
44	307.5	29.1	191	8	ADG00356	Adg00356 Nicotiana
45	306	28.9	303	6	AAE33251	Aae33251 Rice DBF1

## ALIGNMENTS

RESULT 1  
AA97228 standard; protein; 203 AA.  
ID AA97228;  
XX

AC AAY97228;  
XX

DT 19-DEC-2000 (first entry)  
XX

DE Plant transcription factor AP2 DNA-binding domain polypeptide.  
XX

KM AP2; transcription factor; plant metabolism; metabolite; primary;  
XX

KW secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;  
XX

KW food colouring; flavouring; fragrance; antimicrobial; pathogenic;  
XX

KW insecticide; gene expression; mutation.  
XX

OS Catharanthus roseus.  
XX

PN W0200046383-A2.  
XX

PD 10-AUG-2000.  
XX

PF 07-FEB-2000; 2000WC-NL000075.  
XX

PR 05-FEB-1999; 99DK-00000158.  
XX

PR 10-FEB-1999; 99US-0119388P.  
XX

PA (UYLE-) RUDKUNIV LEIDEN.  
XX

PI Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;  
XX

DR WPI; 2000-499380/44.  
XX

DR N-PSDB; AA053745.  
XX

PT Modulating level of metabolites and stress resistance in recombinant  
XX

PT cells for synthesis of plant metabolites such as alkaloids including  
XX

PT terpenoid indole alkaloids, by providing transcription factor to the  
XX

PT cell.  
XX

Disclosure; Page 97-98; 101pp; English.  
XX

Many plant secondary metabolites have value as pharmaceuticals, food  
XX

colourings, flavours and fragrances. Some plant secondary metabolites are  
XX

linked to plant or plant cell defence mechanisms and may confer to the  
XX

plant antimicrobial activity, protection against UV light, herbivores,  
XX

pathogens, insects and nematodes. Plant secondary metabolites such as  
XX

terpenoid indole alkaloids (TIA) represent a class of pharmaceutically  
XX

useful compounds which naturally occur in many plant species. New methods  
XX

are described which modulate the expression of one or more genes involved  
XX

CC in the biosynthesis of plant metabolites or their precursors in plant  
CC cells. The method comprises inserting into a plant cell a sequence  
CC encoding a transcription factor comprising an AP2 DNA-binding domain and  
CC by modifying the expression of that transcription factor. Transcription  
CC factors comprising an AP2 DNA-binding domain are useful as central  
CC regulators of complex metabolite pathways involving numerous target genes  
CC for such transcription factors. This means that the yield of commercially  
CC valuable metabolite compounds can be enhanced and the tolerance of plants  
CC towards exogenous stress factors can be influenced. The method is useful  
CC for modulating the level of one or more metabolites. By providing a  
CC transcription factor to the cell the level of the metabolite is enhanced  
CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to  
CC a cell to which the transcription factor is not provided

SQ Sequence 203 AA:

Query Match 100.0%; Score 1058; DB 3; Length 203;  
Best Local Similarity 100.0%; Pred. No. 1.6e-106;  
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSEITSVSDRFLSLIEEHLSDNSDSSSELTSTEENWEEIFADFLNWSSEIQKGS 60  
DB 1 MSSEITSVSDRFLSLIEEHLSDNSDSSSELTSTEENWEEIFADFLNWSSEIQKGS 60  
QY 61 PSSESCQSNMMAESCOEDSVGTPEPAAGGCGSKDMNRKGVRRRPMWGFPAEIRDPK 120  
DB 61 PSSESCQSNMMAESCOEDSVGTPEPAAGGCGSKDMNRKGVRRRPMWGFPAEIRDPK 120  
QY 121 KGRIRWLGTYETPEDALAYDAAPFMRGAKARLNFPHLIGSNISGPRVNPFRKPPAP 180  
DB 121 KGRIRWLGTYETPEDALAYDAAPFMRGAKARLNFPHLIGSNISGPRVNPFRKPPAP 180  
QY 181 STTSSSSSSSSSSSSSGRKKRRY 203  
DB 181 STTSSSSSSSSSSSSSGRKKRRY 203

## RESULT 2

ADG00355 standard; protein; 227 AA.

XX AC ADG00355;  
XX DT 26-FEB-2004 (first entry)  
XX DE Nicotiana tabacum variant bright yellow protein sequence SEQ ID NO:872.  
XX KW secondary metabolite modulator; biosynthesis; alkaloid; phenylpropanoid;  
XX KM tobacco; Nicotiana tabacum variant bright yellow; Nicotiana tabacum BY;  
XX plant.  
XX OS Nicotiana tabacum.  
XX PN WO2003097790-A2.  
XX PD 27-NOV-2003.  
XX PF 16-MAY-2003; 2003WO-EP050171.  
XX PR 17-MAY-2002; 2002EP-00076973.  
XX PR 04-JUL-2002; 2002EP-0007674.  
XX PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
XX PI (VTTB-) VTT BIOTECHNOLOGY.  
XX PI Inze DG, Goossens A, Oksman-Caldentey K, Haekkinen ST, Laakso IU;  
XX WPI; 2004-022853/02.  
XX DR New isolated polypeptides and polynucleotides useful for modulating the  
XX PT biosynthesis of secondary metabolites (e.g. alkaloids or  
XX PT phenylpropanoids) in an organism or its cell.

PS Claim 2; SEQ ID NO 872; 140pp; English.

XX The present invention describes an isolated polypeptide that modulates  
CC the production of at least one secondary metabolite in an organism, or  
CC its derived cell. The polypeptide is selected from a polypeptide encoded  
CC by a polynucleotide comprising any of the 871 nucleotide sequences given  
CC in the specification. The polypeptides and polynucleotides are useful in  
CC modulating the biosynthesis of secondary metabolites (e.g. alkaloids or  
CC phenylpropanoids) in an organism or its derived cell. The present  
CC sequence is used in the exemplification of the present invention.

SQ Sequence 227 AA:

Query Match 37.8%; Score 400; DB 8; Length 227;  
Best Local Similarity 44.1%; Pred. No. 1e-34;  
Matches 93; Conservative 32; Mismatches 56; Indels 30; Gaps 6;

QY 7 SVSDRFLSLIEEHLSDNSDSSSELTSTEENWEEIFADFLNWS--GSEIQKGS-PS 62  
DB 9 SFSELDPLQSIENHLNLYSD-----FSSEIFSPMSSSNALPMSPESSFGSPS 56  
QY 63 SESECSNMAESCOEDSVGTPEPA-----AAGGCGSKDMNRKGVRRRPMWGF 111  
DB 57 AENSLLDTSLWDENPEETIQLEEKSESSEETKGVVAREKNATQWRRTYGVKRRPMWGF 116  
QY 112 AAETIRDPKKGSRIRWLGTYETPEDALAYDAAPFMRGAKARLNFPHLIGSNISGPRVNP 171  
DB 117 SAETIRDPKKGSRIRWLGTYETPEDALAYDAAPFMRGAKARLNFPHLIGSNIPKPARVT 176  
QY 172 PRKRFPAEPSTTSSSSSSSSSSSGRKKRR 202  
DB 177 ARSRRTSPQ-PSSSSCTSSSEN--GTRKK 204

## RESULT 3

AA97227 standard; protein; 210 AA.

XX AC AA97227;  
XX DT 19-DEC-2000 (first entry)  
XX DE Plant transcription factor AP2 DNA-binding domain polypeptide.  
XX KW AP2; transcription factor; plant metabolism; metabolite; primary;  
XX KM secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;  
XX KW food colouring; flavouring; fragrance; antimicrobial; pathogenic;  
XX KM insecticide; gene expression; modulation.  
XX OS Catharanthus roseus.  
XX PN WO200046383-A2.  
XX PD 10-AUG-2000.  
XX PF 07-FEB-2000; 2000WO-NL000075.  
XX PR 05-FEB-1999; 99DK-00000158.  
XX PR 10-FEB-1999; 99US-0119388P.  
XX PA (UYLE-) RIJKSUNIV LEIDEN.  
XX PI Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;  
XX WPI; 2000-499380/44.  
XX DR N-PSDB; AAA53744.  
XX PT Modulating level of metabolites and stress resistance in recombinant  
XX PT cells for synthesis of plant metabolites such as alkaloids including  
XX PT terpenoid indole alkaloids, by providing transcription factor to the  
XX PT cell.  
XX PS Disclosure; Page 97; 101pp; English.



```
PR      12-OCT-1999;    99US-015836P.  
PR      12-OCT-1999;    99US-015929B.  
PR     13-OCT-1999;    99US-015829A.P  
PR     13-OCT-1999;    99US-015929S.P  
PR     14-OCT-1999;    99US-015932P.  
PR     14-OCT-1999;    99US-015933D.P  
PR     14-OCT-1999;    99US-015933I.P  
PR     14-OCT-1999;    99US-0159637P.  
PR     14-OCT-1999;    99US-0159638P.  
PR     18-OCT-1999;    99US-0159584P.  
PR     21-OCT-1999;    99US-0160741P.  
PR     21-OCT-1999;    99US-0160767P.  
PR     21-OCT-1999;    99US-0160770P.  
PR     21-OCT-1999;    99US-0160814P.  
PR     21-OCT-1999;    99US-0160815P.  
PR     22-OCT-1999;    99US-0160980P.  
PR     22-OCT-1999;    99US-0160981P.  
PR     22-OCT-1999;    99US-0160989P.  
PR     25-OCT-1999;    99US-0161404P.  
PR     25-OCT-1999;    99US-0161405P.  
PR     25-OCT-1999;    99US-0161406P.  
PR     26-OCT-1999;    99US-0161359P.  
PR     26-OCT-1999;    99US-0161360P.  
PR     26-OCT-1999;    99US-0161361P.  
PR     28-OCT-1999;    99US-0161920P.  
PR     28-OCT-1999;    99US-0161922P.  
PR     28-OCT-1999;    99US-016193P.  
PR     29-OCT-1999;    99US-0162142P.
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Query Match          33.8%; Score 358; DB 3; Length 212;  
Best Local Similarity 44.9%; Pred. No.3.4e-30;  
Matches   79; Conservative   24; Mismatches 55; Indels 18; Gaps 5
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```
QY      21 LLSNDDSSSHLTSTEENWEEIFADFLWNGSEBIQRGSPSBSCOSNMASCOEDSV 80  
        :|::||| |:::||| |::||| |::||| |::||| |::||| |::||  
DB     12 ILNDMWSDDLPLSDVDSQC-----MAIVNTLRDAVSAMTPPVPTS-----PAEDK- 59  
  
QY      81 VGTPPEAAAGGCC--KMNRKYGVRRRPPWGCKFAEIRDPKKKGSRILGTYPEDAAL 138  
        ---PPTATSGASHAROKGMQGRGGVRRRPMWKFPAAEIRDRPKKGCARYWLGTETPEDAAV 116  
DB     60 -----PPTATSGASHAROKGMQGRGGVRRRPMWKFPAAEIRDRPKKGCARYWLGTETPEDAAV 116  
  
QY     139 AYDAAAFFMRGAKAPLNFPHILIGSNISGPVVYNRKRFPAEPSTTSSSSSSSSEN 194  
        ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||  
DB     117 AYDRAAFQLRGSKAKLANPFHLIGSCKEYEVRIKRRSRP-EPSVDGLTSEQRES 171
```

```
RESULT 5  
AAG24799  
ID AAG24799 standard; protein; 226 AA.  
XX  
AC AAG24799;  
XX  
DT 17-OCT-2000 (first entry)  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 28611.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.  
XX  
OS Arabidopsis thaliana.  
PN EPI033405-A2.  
PD  
PF 06-SEP-2000.  
PX 25-FEB-2000; 2000EP-00301439.  
PY 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.
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PR	25-MAR-1999;	99US-0126264P;
PR	25-MAR-1999;	99US-0126785P;
PR	01-APR-1999;	99US-0127462P;
PR	06-APR-1999;	99US-0128234P;
PR	08-APR-1999;	99US-0128714P;
PR	16-APR-1999;	99US-0129845P;
PR	19-APR-1999;	99US-0130077P;
PR	21-APR-1999;	99US-0130449P;
PR	23-APR-1999;	99US-0130510P;
PR	28-APR-1999;	99US-0130891P;
PR	30-APR-1999;	99US-0131449P;
PR	30-APR-1999;	99US-0132048P;
PR	30-APR-1999;	99US-0132407P;
PR	04-MAY-1999;	99US-0132484P;
PR	05-MAY-1999;	99US-0132485P;
PR	06-MAY-1999;	99US-0132487P;
PR	06-MAY-1999;	99US-0132487P;
PR	07-MAY-1999;	99US-0132863P;
PR	11-MAY-1999;	99US-0134256P;
PR	14-MAY-1999;	99US-0134218P;
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PR	16-MAY-1999;	99US-0134768P;
PR	19-MAY-1999;	99US-0134941P;
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PR	27-MAY-1999;	99US-0136332P;
PR	28-MAY-1999;	99US-0136782P;
PR	01-JUN-1999;	99US-0137222P;
PR	03-JUN-1999;	99US-0137528P;
PR	04-JUN-1999;	99US-0137502P;
PR	07-JUN-1999;	99US-0137724P;
PR	08-JUN-1999;	99US-0138094P;
PR	10-JUN-1999;	99US-0138540P;
PR	14-JUN-1999;	99US-0138847P;
PR	14-JUN-1999;	99US-0139119P;
PR	16-JUN-1999;	99US-0139452P;
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PR	17-JUN-1999;	99US-0139492P;
PR	18-JUN-1999;	99US-0139454P;
PR	18-JUN-1999;	99US-0139455P;
PR	18-JUN-1999;	99US-0139456P;
PR	18-JUN-1999;	99US-0139457P;
PR	18-JUN-1999;	99US-0139458P;
PR	18-JUN-1999;	99US-0139459P;
PR	18-JUN-1999;	99US-0139460P;
PR	18-JUN-1999;	99US-0139461P;
PR	18-JUN-1999;	99US-0139462P;
PR	18-JUN-1999;	99US-0139463P;
PR	24-JUN-1999;	99US-0140655P;
PR	28-JUN-1999;	99US-0140823P;
PR	29-JUN-1999;	99US-0140991P;
PR	30-JUN-1999;	99US-0141287P;
PR	01-JUL-1999;	99US-0141842P;
PR	01-JUL-1999;	99US-0142154P;
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PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
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PR 18-JUN-1999; 99US-0139458P.  
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PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144684P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
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PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145219P.  
PR 26-JUL-1999; 99US-0145224P.  
PR 27-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
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PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145919P.  
PR 02-AUG-1999; 99US-0146386P.  
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PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147203P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151030P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154799P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158332P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.











Tue Mar 8 08:51:48 2005

us-09-890-782-6.rag

Page 16

Job time : 165 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 21:57.33 / Search time 40 Seconds  
(without alignments)  
488.300 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 1058

Sequence: 1 MBEIISVDRFLSLIEH.....SSSSSSSSSENSGKRRRY 203

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: PIR1:1  
2: PIR2:1  
3: PIR3:1  
4: PIR4:1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356.5	33.7	226	T00409	ethylene-responsive
2	353	33.4	226	T02432	ethylene-responsive
3	338	31.9	243	T51989	ethylene-responsive
4	333	31.5	233	T02590	DNA binding protei
5	328.5	31.0	234	T07686	transcription fact
6	322	30.4	266	T51988	ethylene responsiv
7	312	29.5	225	A85196	EREBP-2 protein [1
8	286.5	27.1	244	B86197	hypothetical prote
9	282.5	26.7	207	T49897	transcription fact
10	266	25.1	161	T07689	transcription fact
11	265.5	25.1	258	T04787	hypothetical prote
12	263	24.9	133	D86175	hypothetical prote
13	263	24.9	218	F84748	probable AP2 domai
14	262.5	24.8	291	T02434	DNA binding protei
15	257.5	24.3	236	B84718	hypothetical prote
16	253	23.9	204	S49031	cadmium-induced pr
17	249.5	23.6	225	T52011	ethylene responsiv
18	248.5	23.5	358	D96579	hypothetical prote
19	245	23.2	603	B71444	probable EREBP-4 -
20	244.5	23.1	212	T48580	hypothetical prote
21	244	23.1	236	T48518	transcription fact
22	241.5	22.8	277	T52020	DNA binding protei
23	241	22.8	300	T52020	ethylene responsiv
24	240.5	22.7	281	T52189	ethylene responsiv
25	240	22.7	314	B86482	protein F5U5.5 [im
26	239.5	22.6	176	T00498	probable AP2 domai
27	237	22.4	259	T52619	TINY-like protein
28	234.5	22.2	204	B86410	protein F3M18.20 [
29	232.5	22.0	218	T01076	transcription fact

30	232.5	22.0	295	2	T00399	probable AP2 domai
31	232	21.9	171	2	T00432	probable AP2 domai
32	232	21.9	196	2	G85435	TINY-like protein
33	232	21.9	263	2	T49870	probable transcrip
34	231.5	21.9	192	2	D96498	RAp2.6 (imported)
35	230.5	21.8	225	2	T02433	DNA binding protei
36	230	21.7	303	2	T04541	hypothetical prote
37	229.5	21.7	262	2	E96747	hypothetical prote
38	227.5	21.5	185	2	D96572	hypothetical prote
39	225.5	21.3	222	2	T52019	ethylene responsiv
40	224	21.2	245	2	B86168	hypothetical prote
41	224	21.2	336	2	B84594	AP2 domain transcr
42	223	21.1	251	2	T01986	Ts11 protein - com
43	222.5	21.0	328	2	G86263	hypothetical prote
44	222	21.0	328	2	G84826	hypothetical prote
45	220	20.8	343	2	T05607	hypothetical prote

#### ALIGNMENTS

RESULT 1  
T00409  
ethylene-responsive transcription factor homolog T13E15.15 - Arabidopsis thaliana  
N/Alternate names: hypothetical protein At2g44840  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004  
C/Accession: T00409; D84883  
R/Roumley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mas  
submitted to the EMBL Data Library, July 1997  
A/Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.  
A/Reference number: Z14146  
A/Accession: T00409  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-226 <ROU>  
A/Cross-references: UNIPROT:Q02167; EMBL:AC002388; NID:G3420042; PID:G2344900  
A/Experimental source: cultivar Columbia  
R/Lin, X.; Kaul, S.; Roumley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.  
euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MID:20083487; PMID:10617197  
A/Accession: D84683  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-226 <STO>  
A/Cross-references: GB:AE002093; NID:G2344900; PIDN:AAC31840.1; GSPDB:GN00139  
C/Genetic:  
A/Gene: At2g44840; T13E15.15  
A/Map position: 2

Query Match 33.7%; Score 356.5; DB 2; Length 226;  
Best Local Similarity 61.1%; Pred. No. 9.6e-24;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;

QY 84 PPEAAGGGS-KDMNRYGVRRPWGKFAEIRDPKKGSRIMLTGTYETPEDALAYD 141  
DB 74 PPAATKASGSHAPQKMGQYRGVRRPWGKFAEIRDPKKGARVIMLTGTYETPEDAAYD 133  
QY 142 AAATFNRGAKARLNFPLIGSNISGVYVNRKRFPAEISTSSSSSSSEN 194  
DB 134 RAATFNRGAKARLNFPLIGSNISGVYVNRKRFPAEISTSSSSSSSEN 185

RESULT 2  
T02432  
ethylene-responsive transcription factor ERFL - common tobacco  
C/Species: Nicotiana tabacum (common tobacco)  
C/Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C/Accession: T02432  
R/Ohme-Takagi, M.; Shinshi, H.

Plant Cell 7, 173-182, 1995  
A>Title: Ethylene-inducible DNA binding proteins that interact with an ethylene response  
A:Reference number: 214671, MUID:95276459, PMID:7756828  
A:Accession: 102432  
A>Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-236 <OHM>  
A:Cross-references: UNIPROT:Q04076, EMBL:D38123, NID:G790359, PIDN:BA07321.1, PID:G1206  
A:Experimental source: strain BY4, tissue-type leaf

Query Match	33.4%	Score 353	DB 2	Length 236
Best Local Similarity	45.3%	Pred. No. 26-23		
Matches	81	Conservative	20	Mismatches 50; Indels 28; Gaps 6
Qy	27	DDSSSELTSTENWEEIFADFLN--WSGSEIOKRGSPSESQCSNMAESCOEDSVVGT	84	
Db	46	DDSDDMWYI-----LKDALNVGMSPNF--SAGEVNSEQ-----RESEIVSP	88	
Qy	85	PEAAAGGCGCKDMNR--YKGYRRRRPMCKFAAETRDPKKXGSRILWTGTYTPEDALAYDAA	143	
Db	89	AETTAAPAAELPRGRHYRGVRRPMPCKFAAETRDPAKNGARWALGTETDEEAAIAADKA	148	
Qy	144	AFNNRGAKARLNPPHILIGNSISGPYVNNRRKFAPEPSTTSSSSSSSSSENGSKRRR	202	
Db	149	AYRRRGKALNPPHILIGNEPEPVAYTKRAASEP-----ASSSENSKRRK	199	

```

RESULT 3
T51989
ethylene responsive element binding factor 2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #ext_change 09-Jul-2004
C:Accession: T51989
R:Fujimoto, S.Y.; Ohta, M.; Usui, A.; Shinshi, H.; Ohme-Takagi, M.
Plant Cell 12, 393-404, 2000
A:Title: Arabidopsis ethylene responsive element binding factors act as transcriptional
A:Reference number: Z25893
A:Accession: T51989
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-243 <FNU>
A:Cross-references: UNIPROT:O80338; EMBL:AB008104; PIDDN:BAA2419.1
C:Genetics:
A:Gene: ERF-2

```

Query Match	31.9%	Score 338	DB 2	Length 243
Best Local Similarity	39.4%	Pred No. 4	3e-22	
Matches	85	Conservative	30	Mismatches 69
			Indels	32
			Gaps	6

  

QY	9	SDRFLLSLIEEHLSDNSDDSSSELTSTEEENBEIIPADFLNMSGSEIOKRG-----	60
Db	9	SDYALLSEITRLLGGGGE---NELRLNESTPSCFTE--SWGGPLKENDSEDMLVYGL	63
QY	61	-PSSSCCSMSAAEQED-----SVGCTPEAALAGGCGSCDMRYKGVARR	106
Db	64	LKDAHFPTSSDLSCLPEFPAVKVPEPTENFTAMEEKPKCALVETAYAKANGYGVARR	123
QY	107	PMGKFAEIRDPKKKGSRIWLTGYETPEBDALAYAAAAFMNGAKARILNPHILISNTSG	166
Db	124	PMGKFAEIRDPKANGARWLTGFETAEBDALAYDIAAFRRKGSALLNLFPLRVNSGEPD	183
QY	167	PVRVNPKRKFPFAEPSTTSSSSSSSSSSSSSGGKKRR	202
Db	184	PVRITSKR--SSSSSSSSSTSSSEN--GLKKRR	214

RESULT 4  
T02590  
DNA binding protein ERBP-2 - (common tobacco)  
C.Species: Nicotiana tabacum (common tobacco)  
C.Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #ext\_change 09-Jul-2004  
C.Accession: T02590  
R.Ohme-takagi, M.; Shinshi, H.

Plant Cell 7, 173-182, 1995  
A:Title: Ethylene-inducible DNA binding proteins that interact with an ethylene responsive element  
A:Reference number: 214671; PMID:95276459; PMID:7756828  
A:Accession: T02590  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-233 <OHM>  
A:Cross-references: UNIPROT:Q04049; EMBL:D38126; NID:9790362; PIDD:BAA07324.1; PID:G1208  
A:Experimental source: strain BY4; tissue-type leaf

[illegible]

RESULT 5  
T07686  
transcription factor Pt14 - tomato (fragment)  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 14-May-1999 #sequence\_rev1sion 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T07686  
R:Zhou, J.; Tang, X.; Martin, G.B.  
submitted to the EMBL Data Library, July 1998  
A:Reference number: Z16094  
A:Accession: T07686  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-234 <ZHO>  
A:Cross-references: UNIPROT:O04680; EMBL:U09255; NID:G3342210; PIDN:AMC50047.1; PID:G3340  
C:Function: transcription factor  
A:Note: binds the GCC box, present in the promoter region of genes encoding pathogenesis  
C:Keywords: DNA binding; transcription factor

	Query Match	31.0%;	Score 38.5;	DB 2;	Length 234;
	Best Local Similarity	47.1%;	Pred. No. 2.8e-21;		
	Matches 73;	Conservative 18;	Mismatches 43;	Indels 21;	Gaps 5
Oy	49	NMGSGEIQKRGSSFSSESCQSNMAESCEQSDSVGTGTPPEAAAGGCSCDKMNR-YKGVRRP	107		
	:::::	-----	----		
Dd	65	NFVAGSV--KSEPREE-----IESSEFS--ESPATTTAAPAETPKGRHYGVQR	113		
Oy	108	WGKFAAEIRDPPKKGSRIWLTGYTEPEDALAIYDAAAFNRRGAQARLNPFHLIGSNTSCP	167		
	:::::			:	:
Dd	114	WGKFAAEIRDPANNGARVWLGTGYTEAEBAALAIYKXAARRGSKAHLPFHRLGLNEPEP	173		
	:::::			:	:
Oy	168	VRVNPBKRFPAPSPSTTSSSSSSSENCGKKRKR	202		
	:::::			:	:
Dd	174	VRVTAKRASPEP-----ASSSGNGSKMR	199		

```

751988      ethylene responsive element binding factor 1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C:Accession: J151988
R: Fujimoto, S.; Ono, M.; Usui, A.; Shishii, H.; Ohme-Takagi, M.
Plant Cell 12, 393-404, 2000
A>Title: Arabidopsis ethylene responsive element binding factors act as transcriptional
A:Reference number: 225893

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A:Accession: T51968  
A:Status: preliminary. translated from GB/EMBL/DDJB  
A:Molecule type: mRNA  
A:Residues: 1-266 <PU>  
A:Cross-references: EMBL:AB008103, PIDD:BA32418.1  
C:Genetics:  
A:Gene: ERF-1

Query Match	30.4%;	Score 322;	DB 2;	Length 266;
Best Local Similarity	36.0%;	Pred. No. 1.2e-20;		
Matches	89;	Conservative 27;	Mismatches 65;	Indels 66;
				Gaps 9;

```

QY      7 SVSDFLLSLIIEHLLSDN---SDSSSELFTST-----EE 38
Db      5 SGGDVAFLESIKRHLIGESEPIIESTASTSVOTGCTGQIKRIVYGNNPSFKLYPCFTE 64
QY      39 NW-----EETADFL-----NW---SGSEIQKRGSPS--SESCQSNMAESC 75
Db      65 SGGDLPLEKNDSEDMLVYGI LNDAPFGCWGPESSSSDEDESSPEPVKIEIPESFAADV 124
QY      76 QEDSVVGFPPPEAAAGCGCKDMNRYGVRRPMPGKFAAEIRDPKKGSRITWLTGYEPED 135
Db      125 PVKKEKTSVSAALVTPAAKCK--HYGVGQORFPGPKPAALERDPADKAGARWLTGFEIYAE 181
QY      136 AALAAVDAAAENNRGAKARLNPPLHLIGSNI SGVPRVNPVRKRFPAEPSTTSSSSSSSSSEN 195
Db      182 AALAAVDRAAFRRMRGSPALLINFLPRVNSGEPDVPRIKSR-----SFSSSSYEN- 229
QY      196 GGRKKRR 202
Db      230 GAKPKGR 236

```

RESULT 7  
AB5196  
ERE2B-2 protein [imported] - Arabidopsis thaliana  
C|Species: Arabidopsis thaliana (mouse-ear cress)  
C|Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C|Accession: AB5196  
R|Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A|Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A|Reference number: AB5001; MUID:20083488; PMID:10617198

	Query March	29.5%	Score 312;	DB 2;	Length 225;
	Best Local Similarity	41.7%;	Pred. No. 7.2e-20;		
	Matches 75; Conservative	19;	Mismatches 46;	Indels 40;	Gaps 4.
QY	23 SDNSDDSSSELTSTEENNEELPADLNMGSGREIQKRGSPSSSCSNMAEACDESYVG	82			
	:   :   :	:   :   :			
Dd	56 SSSSDSDSSSPSVVLETPESFA-----AVDSVPVKKEITSPVS	94			
	:   :   :	:   :   :			
QY	83 TPPEAAAGGCCKDMNRYKYVRRRPWKFAAEIRDPKKKSRIWLGITYETPEDAALAYDA	142			
	:   :   :   :   :   :   :   :	:   :   :   :   :   :   :   :			
Dd	95 AAVTAAG-----KHRYGVQRPMGFPAEIRDPANKGARVMJGTETADALAYDR	147			
	:   :   :   :   :   :   :   :	:   :   :   :   :   :   :   :			
QY	143 AAFFNRGAKALINFLILGSNISGVRYNPVRKRFPABSTTSSSSSSSSSENHGKRRR	202			
	:   :   :   :   :   :   :   :	:   :   :   :   :   :   :   :			
Dd	148 AAFFNRGSRALLNFLRVNGSHPDVRKSKR-----SFSSSNEN-GAPKKR	195			
	:   :   :   :   :   :   :   :	:   :   :   :   :   :   :   :			

RESULT 8  
B86197  
hypoetical protein [imported] - Arabidopsis thaliana  
Cispecies: Arabidopsis thaliana (mouse-ear cress)

CjDate: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
CjAccession: B86197  
RrTheologian: A.; Echter, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;  
ansen, N.F.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000

A. Authors: Hunter, J. L., Jenkins, J., Johnson-Hopson, C., Khan, S., Khaykin, E., Kim, C. A., Li, J. H., Li, Y., Lin, X., Liu, S. X., Liu, Z. A., Luros, J. S., Maltz, R., Marziani-Rizzo, M., Rooney, T., Rowley, D., Sakano, H.  
A. Authors: Salberg, S. L., Schwartz, J. R., Shinn, P., Southwick, A. M., Sun, H., Tallon, K., M., Wu, D., Yu, G., Frazer, C. M., Venter, J. C., Davis, R. W.  
Article: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A. Reference number: A6161; PMID:21016719; PMID:11130712

A:Accession: B86197  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1244 <STO>  
A:Cross-references: UNIPROT:Q9JLND1; GB:AB005172; NID:g8844121; PIDD:AAFA0213.1; GSPDB:G  
C:Genetics:  
A:Map position: 1

Query Match	27.1%	Score 286.5	DB 2	Length 244
Best Local Similarity	33.8%	Pred. No. 1.3e-17		
Matches	72	Conservative	34	Mismatches 56; Indels 51; Gaps 5

  

QY	27	DDSSSELTSTEEN--WEETPADFLNMGSGEITQKGSPPSEBC-----QSNMAESCOED	78
DB	15	ENSSSSSSWSOESFLMEE--SFLHQSDQSFLLSPDNYCCDFAFAPESITIKEGKEA	71
QY	79	SVWGPPPALAAGGCGSKDMNRYKGVRRPQWCKFPAEITDPKKKSRIWLTGYEPEDAL	138
DB	72	TVAABEEBKS-----YRGVRRKRPWCKFPAEITDSTRKIGRWLGTFTDEAALL	120
QY	139	AYDAAAFNMGAKARLNP-----HLIGSNISGVR	169
DB	121	AYDQAAFLKSLAVLNFPADVAVEESLRKMENVNLNDESPVIALKRGHSMRNPGRGKK	180
QY	170	VNPKRRPAPRPESTSSSSSSSSSSSGGRKKR	202
DB	181	SSSGSTLTSPSSSSSYSSSSSSSSSLSRKKQ	213

RESULT 9  
 T49897  
 transcription factor-like protein - *Arabidopsis thaliana*  
 N|Alternate names: protein 121L290  
 C|Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C|Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
 C|Accession: T49897  
 R|Beyan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; L  
 submitted to the Protein Sequence Database, April 2000  
 A|Reference number: Z24493

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A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <BEV>
A:Cross-references: UNIPROT:O9LY05; EMBL:AL163912; GSPDB:GN00063; ATSP:T211.290
A:Experimental source: cultivar Columbia; BAC clone T211
C:Genetics:
A:Gene: ATSP:T211.290
A:Map position: 5

Query Match      26.7%  Score 282.5;  DB 2;  Length 207;
      Best Local Similarity 38.0%;  Pred. No. 2.4e-17;
      Matches 78;  Conservative 20;  Mismatches 74;  Indels 33;  Gaps 5;

QY      4  ELIVSRFL-----LSLIEHLLSDNSDDSSSLTSGEENWEETPADFLWMS 51
DB      19  EDLVLCDFMDDPDPDASFVSGWLCIEHNVKQBPDSVVDPPDSFVNEFLVQEGSSSS 78

QY      52  GSEIQKRGSPSSSCQSNMAESCQEDSVGCTPPEAAGGCGCDMNRYKGVRRRRPKGF 111
DB      79  SPELNS-SSSYETEDQSYKKAERFEE-----VDARYRCVRRRRPKGF 121

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 22:06:15 ; Search time 130 Seconds

(without alignments)  
512.254 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 1058

Sequence: 1 MSEELISVSDRFLSLIEH.....SSSSSSSSSSSGRRKKRRY 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 138539 seqs, 32804528 residues

Total number of hits satisfying chosen parameters: 138539

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	356.5	33.7	226	US-10-225-068-128	Sequence 128, App
2	356.5	33.7	226	US-10-374-780A-6	Sequence 6, App1
3	356.5	33.7	226	US-10-412-6-99B-28	Sequence 28, App1
4	356.5	33.6	202	US-10-424-599-175489	Sequence 175489,
5	345	32.6	282	US-10-374-780A-503	Sequence 503, App
6	338	31.9	243	US-09-533-029-34	Sequence 34, App1
7	338	31.9	243	US-09-934-455-416	Sequence 416, App
8	338	31.9	243	US-10-374-780A-2074	Sequence 2074, App
9	338	31.9	243	US-10-412-6-99B-670	Sequence 670, App
10	338	31.9	243	US-10-412-6-99B-1832	Sequence 1832, App
11	331.5	31.3	156	US-10-425-114-41687	Sequence 41687, A
12	331.5	31.3	156	US-10-424-599-208822	Sequence 208822,
13	330.5	31.2	311	US-10-425-114-43402	Sequence 43402, A

14	324	30.6	268	10	US-09-533-029-18
15	324	30.6	268	10	US-09-934-455-2
16	324	30.6	268	15	US-10-225-068-196
17	324	30.6	268	15	US-10-374-780A-10
18	324	30.6	268	15	US-10-412-6-99B-38
19	324	30.6	268	17	US-10-495-918-102
20	322.5	30.5	318	16	US-10-437-963-183672
21	322	30.4	328	16	US-10-437-963-1191950
22	316.5	29.9	318	16	US-10-437-963-145941
23	309.5	29.3	147	15	US-10-424-599-242420
24	309.5	29.3	205	15	US-10-424-599-146343
25	306	28.9	240	15	US-10-424-599-220299
26	306	28.9	303	16	US-10-437-963-118008
27	302.5	28.6	199	15	US-10-424-599-214365
28	302.5	28.6	203	15	US-10-425-114-36689
29	299	28.3	195	15	US-10-424-599-173756
30	299	28.3	211	15	US-10-425-114-56040
31	298.5	28.2	231	14	US-10-122-822-1
32	297.5	28.1	259	15	US-10-374-780A-501
33	297.5	28.1	229	15	US-10-412-6-99B-1000
34	294	27.8	271	15	US-10-310-154-476
35	292	27.6	240	15	US-10-425-114-39862
36	292	27.6	344	16	US-10-437-963-152032
37	286.5	27.1	244	15	US-10-402-366-2
38	286.5	27.1	244	15	US-10-225-068A-474
39	286.5	27.1	244	15	US-10-225-067-106
40	286.5	27.1	244	15	US-10-374-780A-2876
41	285.5	27.0	201	15	US-10-225-066A-788
42	285.5	27.0	201	15	US-10-374-780A-2230
43	285.5	27.0	201	15	US-10-412-6-99B-50
44	285.5	27.0	201	15	US-10-412-6-99B-1726
45	285	26.9	135	16	US-10-767-701-36377

#### ALIGNMENTS

Sequence 18, App1  
Sequence 2, App1  
Sequence 196, App  
Sequence 10, App1  
Sequence 38, App1  
Sequence 102, App  
Sequence 183672,  
Sequence 121950,  
Sequence 145941,  
Sequence 242420,  
Sequence 146343,  
Sequence 220299,  
Sequence 118008,  
Sequence 214365,  
Sequence 36689, A  
Sequence 173756,  
Sequence 56040, A  
Sequence 501, App  
Sequence 1000, App  
Sequence 476, App  
Sequence 39862, A  
Sequence 152032,  
Sequence 2, App1  
Sequence 474, App  
Sequence 106, App  
Sequence 2876, App  
Sequence 788, App  
Sequence 2230, App  
Sequence 50, App1  
Sequence 1726, App  
Sequence 36377, A

RESULT 1  
US-10-225-068-128  
Sequence 128, Application US/10225068  
Publication No. US20030217383A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Heard, Jacqueline E.  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Adam, Luc J.  
APPLICANT: Dubell, Arnold T.  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Pineda, Omaria  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Brown, Pierre E.  
TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND  
POLYPEPTIDES IN PLANTS  
FILE REFERENCE: 514442002040  
CURRENT APPLICATION NUMBER: US/10/225,068  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 128  
LENGTH: 226  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
FEATURE:

NAME/KEY: DOMAIN  
LOCATION: (89)...(157)  
OTHER INFORMATION: Conserved domain  
US-10-225-068-128

Query Match 33.7%; Score 356.5; DB 15; Length 226;  
Best Local Similarity 61.1%; Pred. No. 7.6e-27;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;

Qy 84 PPEAAGGCS--KDNRRKGVRRPVGKFAAERDPKKKSRIMLGTETEDAAAYD 141  
Db 74 PPATKASGSHAPQKMQYRGVRRPWGKFAAERDPKNGARVWLGTETEDAAVAYD 133  
Qy 142 AAFFNMGAKARLNFPHLIGSNISGVRVNPVRKRPAPSTSSSSSSSEN 194  
Db 134 RAAFQLRGSKAKLNFPHLIGSCYEPVRI RPRRSP-EPVSVDLTSEQRES 185

## RESULT 2

US-10-374-780A-6  
Sequence 6, Application US/10374780A  
Publication No. US20040019927A1  
GENERAL INFORMATION:  
APPLICANT: Sherman, Bradley K  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Heard, Jacqueline E  
APPLICANT: Haake, Volker  
APPLICANT: Creelman, Robert A  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Adam, Luc J  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddie, James  
APPLICANT: Brown, Pierre E  
APPLICANT: Pilgrim, Marsha L  
APPLICANT: Dubell III, Arnold T  
APPLICANT: Pineda, Omayra  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
FILE REFERENCE: MBI-0047 CIP  
CURRENT APPLICATION NUMBER: US/10/374, 780A  
CURRENT FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: 09/837,944  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/934,455  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
PRIOR APPLICATION NUMBER: 10/225,066  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,067  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,068  
PRIOR FILING DATE: 2002-08-09  
NUMBER OF SEQ ID NOS: 2906  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 6  
LENGTH: 226  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
OTHER INFORMATION: G22 (conserved domain in AA coordinates: 89-157)  
US-10-374-780A-6

Query Match 33.7%; Score 356.5; DB 15; Length 226;  
Best Local Similarity 61.1%; Pred. No. 7.6e-27;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;

Qy 84 PPEAAGGCS--KDNRRKGVRRPVGKFAAERDPKKKSRIMLGTETEDAAAYD 141  
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Qy 142 AAFFNMGAKARLNFPHLIGSNISGVRVNPVRKRPAPSTSSSSSSSEN 194  
Db 134 RAAFQLRGSKAKLNFPHLIGSCYEPVRI RPRRSP-EPVSVDLTSEQRES 185

## RESULT 3

US-10-412-699B-28  
Sequence 28, Application US/10412699B  
Publication No. US20040045049A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Zhang, James  
APPLICANT: Fromm, Michael E.  
APPLICANT: Heard, Jacqueline E.  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Adam, Luc J.  
APPLICANT: Brown, Pierre E.  
APPLICANT: Pineda, Omayra  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddie, James S.  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Samaha, Raymond R.  
APPLICANT: Pilgrim, Marsha L.  
APPLICANT: Creelman, Robert A.  
APPLICANT: Dubell, Arnold N.  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Kumimoto, Roderick  
APPLICANT: Sherman, Bradley K.  
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
FILE REFERENCE: MBI-0048CIP  
CURRENT APPLICATION NUMBER: US/10/412,699B  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: 09/394,519  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: 09/489,376  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: 09/506,720  
PRIOR FILING DATE: 2000-02-17  
PRIOR APPLICATION NUMBER: 09/533,030  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,392  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,029  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/532,591  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,648  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/713,994  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: 09/819,142  
PRIOR FILING DATE: 2001-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2011  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 28  
LENGTH: 226  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
OTHER INFORMATION: G22  
US-10-412-699B-28

Query Match 33.7%; Score 356.5; DB 15; Length 226;  
Best Local Similarity 61.1%; Pred. No. 7.6e-27;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;

[illegible]

RESULT 4  
US-10-42.

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: Sequence 175489, Application US/10424539
: Publication No. US20040031072A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa Thomas J
: APPLICANT: Kovalic David K
: APPLICANT: Zhou Yihua
: APPLICANT: Cao Yongwei
: TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53223)B
: CURRENT APPLICATION NUMBER: US/10/424,599
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ. ID NOS: 285684
: SEQ. ID NO. 175489
: LENGTH: 202
: TYPE: PRT
: ORGANISM: Glycine max
: FEATURE:
: OTHER INFORMATION: Clone ID: PAT_MRT3847_129485C.1 pep
: US-10-424-599-175489

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Query Match	33.6%	Score 356;	DB 15;	length 202;
Best Local Similarity	41.3%	Pred. No. 7.4e-27;		
Matches	83;	Conservative	29;	Mismatches 55;
			Indels	34;
			Gaps	5;

[illegible]

RESULT 5  
US-10-37

Sequence 503, Application us/10374780A  
Publication No. US202040019927A1  
GENERAL INFORMATION:  
APPLICANT: Sherman, Bradley K  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Heard, Jacqueline E  
APPLICANT: Haake, Volker  
APPLICANT: Creelman, Robert A  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Adam, Luc J  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddie, James  
APPLICANT: Brown, Pierre E  
APPLICANT: Pilgrim, Marsha L  
APPLICANT: Dubeil III, Arnold T  
APPLICANT: Pineda, Omaira  
APPLICANT: Yu, Guo-Liang

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1  TITLE OR INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
2  FILE REFERENCE:  M81-0047 CIP
3  CURRENT APPLICATION NUMBER:  US/10/374,780A
4  PRIOR FILING DATE:  2003-02-25
5  PRIOR APPLICATION NUMBER:  09/837,944
6  PRIOR FILING DATE:  2001-04-18
7  PRIOR APPLICATION NUMBER:  60/310,847
8  PRIOR FILING DATE:  2001-08-09
9  PRIOR APPLICATION NUMBER:  09/934,455
10 PRIOR FILING DATE:  2001-08-22
11 PRIOR APPLICATION NUMBER:  60/336,049
12 PRIOR FILING DATE:  2001-11-19
13 PRIOR APPLICATION NUMBER:  60/338,692
14 PRIOR FILING DATE:  2001-12-11
15 PRIOR APPLICATION NUMBER:  10/111,468
16 PRIOR FILING DATE:  2002-06-14
17 PRIOR APPLICATION NUMBER:  10/225,066
18 PRIOR FILING DATE:  2002-08-09
19 PRIOR APPLICATION NUMBER:  10/225,067
20 PRIOR FILING DATE:  2002-08-09
21 PRIOR APPLICATION NUMBER:  10/225,068
22 PRIOR FILING DATE:  2002-08-09
23 NUMBER OF SEQ ID NOS: 2906
24 SOFTWARE: PatentIn version 3.2
25 SEQ ID NO 503
26 LENGTH: 282
27 TYPE: PRT
28 ORGANISM: Mesembryanthemum crystallinum
29 FEATURE:
30 OTHER INFORMATION: Orthologous to G28
31 US-10-374-780A-503

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OTHER INFORMATION: Orthologous to G28;  
US-10-374-780A-503

Query Match	32.6%	Score 345;	DB 15;	Length 282;
Best Local Similarity	40.5%	Pred. No. 1.4e-25;		
Matches	96;	Conservative	22;	Mismatches 63;
				Indels 56;
				Gaps 10;

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QY SDFEFLLSLEENHLS-----NDDSS-----SELTSTWEN 39
   ||| :||| |||
Db SDPAVLESIRRHLEDMDPRACAPAITTGGSGFVTHRNSFSYLPCLTDMGELPLKEDD 68
   ||| :||| |||
QY WEETI-----ADFLNW-----SGSEIORGSBSHSCOSNMAESCDESVVGTP-PEAA 88
   ||| :||| |||
Db SEDMWLFGVLROAVHTGMSPQSGS-SGSGSPATVTVAPEVV-----DSPVSFAIVRV 122
   ||| :||| |||
QY AGC-----GCSDXMRYYKGVRRRPWGKPAAEIRDPKKKGSIWTCTETPEDAALAYDA 144
   ||| :||| |||
Db AGGEAFVAAPAPARGKIYRCVRRRPMGKFAAEIRDPARKGAFAVMGTGETAEDALAYDRA 181
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QY AFNMRCAKARLNPPHLIGSNISGPVRVNPKRFPABEPTTTTTSSSSSSSENSSGCRK 200
   ||| :||| |||
Db AEFMRSSKLLNLPRLVNSGEDPVPRIITSKSSP-ERSVSSSSSESASPKR--RKK 224
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RESULT 6  
US-09-53

Sequence 34, Application US/09533029  
Publication No. US20030046723A1  
GENERAL INFORMATION:  
APPLICANT: Heard, Jacqueline  
APPLICANT: Brown, Pierre  
APPLICANT: Reichmann, Jose-Luis  
APPLICANT: Keddie, James  
APPLICANT: Pineda, Omaira  
APPLICANT: Adam, Luc  
APPLICANT: Shamah, Raymond  
APPLICANT: Zhang, James  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Pilgrim, Marsha  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Reuber, Lyne  
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES  
FILE REFERENCE: MBI-010

Query Match	31.9%;	Score 338;	DB 10;	Length 243;
Best Local Similarity	39.4%;	Pred. No. 5.7e-25;		
Matches	85;	Conservative	30;	Mismatches 69;
			Indels	32;
			Gaps	6

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// PRIOR FILING DATE: 2001-04-18
// PRIOR APPLICATION NUMBER: 60/310,847
// PRIOR FILING DATE: 2001-08-09
// PRIOR APPLICATION NUMBER: 09/934,455
// PRIOR FILING DATE: 2001-08-22
// PRIOR APPLICATION NUMBER: 60/336,049
// PRIOR FILING DATE: 2001-11-19
// PRIOR APPLICATION NUMBER: 60/338,692
// PRIOR FILING DATE: 2001-12-11
// PRIOR APPLICATION NUMBER: 10/171,468
// PRIOR FILING DATE: 2002-06-14
// PRIOR APPLICATION NUMBER: 10/225,066
// PRIOR FILING DATE: 2002-08-09
// PRIOR APPLICATION NUMBER: 10/225,067
// PRIOR FILING DATE: 2002-08-09
// PRIOR APPLICATION NUMBER: 10/225,068
// PRIOR FILING DATE: 2002-08-09
// NUMBER OF SEQ ID NOS: 2906
// SOFTWARE: PatentIn version 3.2
// SEQ ID NO 2074
// LENGTH: 243
// TYPE: prt
// ORGANISM: Arabidopsis thaliana
// FEATURE:
// OTHER INFORMATION: G1006 Paralogous to G28
// US-10-374-780A-2074

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Query Match	31.9%;	Score 338;	DB 15;	Length 243;
Best Local Similarity	39.4%;	Pred. NO. 5.7e-25;		
Matches	85;	Conservative	30;	Mismatches 69;
				Indels 32;
				Gaps 6;

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Qy 9 SDRPILSLIEEHLISNSDDSSSELTSTSENMEEIFADPLNMSGEIQRGS----- 60
Db 9 SDVALLESTRHLLGGGGE---NELKINESTSSCTE--SWGLPLKENDSEMDLVYGL 63
Qy 61 -PSESCQSNMAESQCED-----SVGTPEPAAAGGCGSKDMNRKYGVRR 106
Db 64 LKDAFHDPDTSSDLSCIFDPBAVKVPTENFTAMEBKPKCALPVETAKAHYGVQR 122
Qy 107 PKCKFAEITDPKKKSSRTMLGYTEPEPDALALAYDAAANMGAGARLNFPHLISNLSG 166
Db 124 PWGFAAEIRDPKKNARVWLGFTEAEDALALAYDIAAARMKGSBALNFPILRVNSGPD 183
Qy 167 PVRVNPKRFPAPSTSTSSSSSSSSSSSSSGCRKRK 202
Db 184 PVRITSKR---SSSSSSSSSSSSSTSSSEN--GLTKRR 214

RESULT 9
US-10-412-699B-670
Sequence 670. Application US/10412699B
Publication No. US20040045049A1
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: Zhang, James
APPLICANT: Fromm, Michael E.
APPLICANT: Heard, Jacqueline E.
APPLICANT: Riechmann, Jose Luis
APPLICANT: Adam, Luc J.
APPLICANT: Broun, Pierre E.
APPLICANT: Pineda, Omalra
APPLICANT: Reuber, T. Lynne
APPLICANT: Keddie, James S.
APPLICANT: Yu, Guo-liang
APPLICANT: Utang, Cai-Zhong
APPLICANT: Samaha, Raymond R.
APPLICANT: Pilgrim, Marsha L.
APPLICANT: Creelman, Robert A.
APPLICANT: Dubell, Arnold N.
APPLICANT: Ratcliffe, Oliver
APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBI-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/532,591
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,648
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR FILING DATE: 2001-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: PatentIn version 3.2
SEQ ID NO 670
LENGTH: 243
TYPE: PRT
ORGANISM: Arabidopsis thaliana

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[illegible]

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1832
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-412-699B-1832

Query Match
Best Local Similarity 31.9%; Score 338; DB 15; Length 243;
Best Local Similarity 39.4%; Pred. No. 5.7e-25;
Matches 85; Conservative 30; Mismatches 69; Indels 32; Gaps 6;

QY 9 SDRFLSLIEHLSDNSDSSSELTSTEENWEIIPADFLWNGSEIQKGS-----60
DB 9 SDYALLESITRHLGGGGE---NELRLNTESTPSSCFTE--SWGGLPLKENDSEDMLVYGL 63
QY 61 -SSSECCQSNMAESQED-----SVVGTPEAAAGCGCKDMRRYGVRR 106
DB 64 LKDAFHFDITSSDLSCLFDPFAVKVPEPTENFTAMEEKPKKALPVETAVKAKHYGVRR 123
QY 107 PMGKFAAEIRDPKKGSRIMLGTYETPEDALAYDAAAENMGAKARLNFPHLIGSNISG 166
DB 124 PMGKFAAEIRDPKKGARVWLGTFTAEADALAYDIAAFRMRGSRALLNPLRVNSGEDP 183
QY 167 PVRVNRKRPFAEPSTSSSSSSSSSSSGRKKR 202
DB 184 PVRITSKR---SSSSSSSSSSSTSSSEN--GLTKRR 214

RESULT 11
US-10-425-114-41687
; Sequence 41687, Application US/10425114
; Publication No. US20040034888A1
GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41687
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB25-108-B7_FLI.pep
US-10-425-114-41687

Query Match
Best Local Similarity 31.9%; Score 338; DB 15; Length 248;
Best Local Similarity 39.4%; Pred. No. 5.8e-25;
Matches 85; Conservative 30; Mismatches 69; Indels 32; Gaps 6;

QY 9 SDRFLSLIEHLSDNSDSSSELTSTEENWEIIPADFLWNGSEIQKGS-----60
DB 14 SDYALLESITRHLGGGGE---NELRLNTESTPSSCFTE--SWGGLPLKENDSEDMLVYGL 68
QY 61 -SSSECCQSNMAESQED-----SVVGTPEAAAGCGCKDMRRYGVRR 106
DB 69 LKDAFHFDITSSDLSCLFDPFAVKVPEPTENFTAMEEKPKKALPVETAVKAKHYGVRR 128
QY 107 PMGKFAAEIRDPKKGSRIMLGTYETPEDALAYDAAAENMGAKARLNFPHLIGSNISG 166
DB 129 PMGKFAAEIRDPKKGARVWLGTFTAEADALAYDIAAFRMRGSRALLNPLRVNSGEDP 188
QY 167 PVRVNRKRPFAEPSTSSSSSSSSSGRKKR 202
DB 184 PVRITSKR---SSSSSSSSSSSTSSSEN--GLTKRR 214
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DB 189 PVRITSKR---SSSSSSSSSSSTSSSEN--GLTKRR 219

RESULT 12
US-10-424-599-208822
; Sequence 208822, Application US/10424599
; Publication No. US20040031072A1
GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 208822
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_30595C.1.pep
US-10-424-599-208822

Query Match
Best Local Similarity 31.3%; Score 331.5; DB 15; Length 156;
Best Local Similarity 52.1%; Pred. No. 1.4e-24;
Matches 73; Conservative 14; Mismatches 38; Indels 15; Gaps 3;

QY 30 SSELSTEENWEIIPADFLWNGSEI---QKRGSSSSSCQSNK-ASCCQEDSVYGR 84
DB 2 SSTTSDSCYCLEIQOYLLHNDSTILTPQAFPPSPSHSSSDASVHFHPSEADHVNAP 61
QY 85 PEAAAGCGCKDMRRYGVRRPMGKFAAEIRDPKKGSRIMLGTYETPEDALAYDAAA 144
DB 62 PK-----RRYRGVRRPMGKFAAEIRDPKKGSRVWLGTVNEEADALAYDKAA 111
QY 145 FNRMGAKARLNFPHLIGSN 164
DB 112 FNRMGQKAKLNFPHLIGSV 131

RESULT 13
US-10-425-114-43402
; Sequence 43402, Application US/10425114
; Publication No. US20040034888A1
GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43402
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700237304_FLI.pep
US-10-425-114-43402

Query Match
Best Local Similarity 31.2%; Score 330.5; DB 15; Length 311;
Best Local Similarity 36.9%; Pred. No. 4.4e-24;
Matches 90; Conservative 29; Mismatches 54; Indels 71; Gaps 11;

QY 9 SDRFLSLIEHLSDNSDSSSELTSTEENWEIIPADFLWNGS-----53
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Db 42 SETSVLDTIRQHLL---EBPAAAEARPADESPGSLVAD---QWSSSLFRTDDADDMWVFG 96
Qy 54 EIQKR-----GS-----PSSSCOSNSMAESCOEDSVVGT-----84
Db 97 VLQDAFAYGWLPGDSFVHVXPEPVRSPPSSSYHPCSYD---GSPFCGLDPEPLTPGTT 153
Qy 85 -----PEAAAGGCSKDMNRKGVRRPMPGKFAAEIRDPKKGSRIWLTGYETPEPAAL 138
Db 154 TPGRGEBAANAARAGK---HYRGVRORPMGKFAAEIRDPKRNARVWLGTDTAEADAL 210
Qy 139 AYDAAAFNMKGAKARLNFPHLIGSNISGPVVRNPKRFPAPESPSTSSSSSSSSSSSSGGR 198
Db 211 AYRAAAYRMKGRSRLNLFPLRIG---SGDKRPSRA---PPEPATSSDSSSSA---SGSH 260
Qy 199 KKR 202
Db 261 KRRK 264

RESULT 14
US-09-533-029-18
; Sequence 18, Application US/09533029
; Publication No. US20030046723A1
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddle, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 268
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G28
US-09-533-029-18

Query Match 30.6%; Score 324; DB 10; Length 268;
Best Local Similarity 36.0%; Pred. No. 1.6e-23;
Matches 91; Conservative 27; Mismatches 69; Indels 66; Gaps 9;

Qy 1 MSEEIISVSDRFLSLIEHLSDN-----SDSSSELSTST-----36
Db 1 MSMTADSQSDYAFLESIRRLHGESEPILESTYASSVTGSCVYGQSIKPYGNNPFSKL 60
Qy 37 -----EENW-----EELFADFL-----NW-----SGSEIQKRGSPS--SESCQSN 69
Db 61 YPCFTESWGDLPKENDSEDMLVYGLINDAFHGWEPSSSSSDDEDRSSPFSVKIETPESF 120
Qy 70 SMAESCOEDSVGTPEPAAAGGCSKDMNRKGVRRPMPGKFAAEIRDPKKGSRIWLTGT 129
Db 121 AAVDSVPVKKEKTSFVSAATAAGK---HYRGVRORPMGKFAAEIRDPKRNARVWLGT 177
Qy 130 YETPEDAALAYDAAAFNMKGAKARLNFPHLIGSNISGPVVRNPKRFPAPESPSTSSSSSS 189
Db 178 FETAEADALAYDAAAFNMKGRSRLNLFPLRVNSGEPDPVRIKSKR-----SSFS 226
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Qy 190 SSENSEGGRRKR 202
Db 227 SSNEN-GAPKKR 238

RESULT 15
US-09-934-455-2
; Sequence 2, Application US/09934455
; Publication No. US20030121070A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Luc
; APPLICANT: Creelman, Robert
; APPLICANT: Dubell, Arnold
; APPLICANT: Heard, Jacqueline
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Keddle, James
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pineda, Omaira
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV
; FILE REFERENCE: MBI-0025
; CURRENT APPLICATION NUMBER: US/09/934,455
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: MBI-0022
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: MBI-0023
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 268
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-09-934-455-2

Query Match 30.6%; Score 324; DB 10; Length 268;
Best Local Similarity 36.0%; Pred. No. 1.6e-23;
Matches 91; Conservative 27; Mismatches 69; Indels 66; Gaps 9;

Qy 1 MSEEIISVSDRFLSLIEHLSDN-----SDSSSELSTST-----36
Db 1 MSMTADSQSDYAFLESIRRLHGESEPILESTYASSVTGSCVYGQSIKPYGNNPFSKL 60
Qy 37 -----EENW-----EELFADFL-----NW-----SGSEIQKRGSPS--SESCQSN 69
Db 61 YPCFTESWGDLPKENDSEDMLVYGLINDAFHGWEPSSSSSDDEDRSSPFSVKIETPESF 120
Qy 70 SMAESCOEDSVGTPEPAAAGGCSKDMNRKGVRRPMPGKFAAEIRDPKKGSRIWLTGT 129
Db 121 AAVDSVPVKKEKTSFVSAATAAGK---HYRGVRORPMGKFAAEIRDPKRNARVWLGT 177
Qy 130 YETPEDAALAYDAAAFNMKGAKARLNFPHLIGSNISGPVVRNPKRFPAPESPSTSSSSSS 189
Db 178 FETAEADALAYDAAAFNMKGRSRLNLFPLRVNSGEPDPVRIKSKR-----SSFS 226
Qy 190 SSENSEGGRRKR 202
Db 227 SSNEN-GAPKKR 238
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Job time : 131 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2005, 21:58:04 ; Search time 43 Seconds

(without alignments)  
352,413 Million cell updates/sec

Title: US-09-890-782-6

Sequence: 1 MSSEIISVDRFLSLIEH.....SSSSSSSSSSSGRRKRRY 203

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/1/aa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/1/aa/6A COMB.pep.\*  
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6: /cgn2\_6/prodata/1/aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	31.9	243	4	US-09-533-029-34 Sequence 34, Appl
2	324	30.6	268	4	US-09-533-029-18 Sequence 18, Appl
3	298.5	28.2	231	4	US-09-202-161B-1 Sequence 1, Appl
4	274	25.9	69	3	US-08-912-272-18 Sequence 16, Appl
5	274	25.9	69	3	US-09-026-039-18 Sequence 18, Appl
6	266	25.1	60	3	US-09-300-672-9 Sequence 2, Appl
7	266	25.1	161	4	US-09-202-161B-2 Sequence 11, Appl
8	262	24.8	61	2	US-08-949-603-11 Sequence 11, Appl
9	262	24.8	61	2	US-08-706-370A-11 Sequence 11, Appl
10	262	24.8	61	2	US-08-949-580-11 Sequence 11, Appl
11	262	24.8	61	2	US-08-950-172A-11 Sequence 11, Appl
12	262	24.8	61	4	US-09-198-119C-11 Sequence 11, Appl
13	262	24.8	61	4	US-09-601-802D-11 Sequence 11, Appl
14	262	24.8	63	4	US-09-601-802D-134 Sequence 134, Appl
15	258	24.4	69	3	US-08-912-272-17 Sequence 17, Appl
16	258	24.4	69	3	US-08-026-039-17 Sequence 17, Appl
17	254	24.0	69	3	US-09-202-161B-25 Sequence 25, Appl
18	252	23.8	69	3	US-08-912-272-20 Sequence 20, Appl
19	252	23.8	69	3	US-09-026-039-20 Sequence 20, Appl
20	251.5	23.8	248	4	US-09-533-029-22 Sequence 22, Appl
21	247	23.3	59	4	US-09-202-161B-26 Sequence 26, Appl
22	244.5	22.7	387	4	US-09-640-211A-810 Sequence 810, Appl
23	240.5	22.7	375	4	US-09-533-029-12 Sequence 12, Appl
24	239	22.6	364	3	US-08-894-731-4 Sequence 4, Appl
25	237	22.4	243	4	US-09-640-211A-1140 Sequence 1140, Appl
26	235	22.2	243	4	US-09-640-211A-761 Sequence 761, Appl
27	232.5	22.0	501	4	US-09-640-211A-1027 Sequence 1027, Appl

28	232	21.9	171	4	US-09-533-029-82 Sequence 82, Appl
29	228.5	21.6	68	3	US-08-912-272-24 Sequence 24, Appl
30	228.5	21.6	68	3	US-09-026-039-24 Sequence 24, Appl
31	226.5	21.4	68	3	US-08-912-272-21 Sequence 21, Appl
32	226.5	21.4	68	3	US-08-912-272-25 Sequence 25, Appl
33	226.5	21.4	68	3	US-09-026-039-21 Sequence 21, Appl
34	226.5	21.4	68	3	US-09-026-039-25 Sequence 25, Appl
35	225.5	21.3	59	3	US-09-300-672-7 Sequence 7, Appl
36	225.5	21.3	68	3	US-08-912-272-22 Sequence 22, Appl
37	225.5	21.3	68	3	US-09-026-039-22 Sequence 22, Appl
38	224	21.2	167	4	US-09-640-211A-838 Sequence 838, Appl
39	222.5	21.0	59	3	US-09-300-672-10 Sequence 10, Appl
40	222.5	21.0	328	4	US-09-964-850-4 Sequence 4, Appl
41	222.5	21.0	328	4	US-09-964-850-6 Sequence 6, Appl
42	222.5	21.0	328	4	US-10-102-949-7 Sequence 7, Appl
43	222.5	21.0	328	4	US-10-102-949-11 Sequence 11, Appl
44	222	21.0	328	4	US-09-300-672-2 Sequence 2, Appl
45	221.5	20.9	68	3	US-08-912-272-23 Sequence 23, Appl

# ALIGNMENTS

## RESULT 1

US-09-533-029-34  
Sequence 34, Application US/09533029  
Patent No. 666446  
GENERAL INFORMATION:  
APPLICANT: Heard, Jacqueline  
APPLICANT: Broun, Pierre  
APPLICANT: Riechmann, Jose-Luis  
APPLICANT: Keddie, James  
APPLICANT: Pineda, Omaira  
APPLICANT: Adam, Luc  
APPLICANT: Samaha, Raymond  
APPLICANT: Zhang, James  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Piggitt, Marsha  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Reuber, Lynne  
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES  
FILE REFERENCE: MBI-010  
CURRENT APPLICATION NUMBER: US/09/533,029  
CURRENT FILING DATE: 2000-03-22  
EARLIER APPLICATION NUMBER: 60/125,814  
EARLIER FILING DATE: 1999-03-23  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 34  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
OTHER INFORMATION: G1006  
US-09-533-029-34

Query Match 31.9%; Score 338; DB 4; Length 243;

Best Local Similarity 39.4%; Pred. No. 3.3e-30; Matches 85; Conservative 30; Mismatches 69; Indels 32; Gaps 6;

QY 9 SDRFLSLIEHLINSDDSSSELTSTERNNEITADFLNMGSGSIQRGS-----60  
DB 9 SDYALLSITRHLGGGGE---NELRLNSTPSSCFTE--SWGGLPKENDSEDMUYGL 63  
QY 61 -PSESQSNMSESCOE-----SVGTPEAAAGGCGCKDMNRYKGVRR 106  
DB 64 LKAAFPDTRSSSLCLFDPFAVKVPTENFTMEKKPKKAIIVTETAQAKHYRGROR 123  
QY 107 PWCKFAEIRDPKKKSRILGTYETPEDAALAYDAAFNMGAKALNPHILGNSISG 166  
DB 124 PWCKFAEIRDPKNGARVWLGTFTABDAALAYDIAAFRMGSRALNPFRLVNSGEPD 183

QY 167 PVRNPRKRPAPETSTSSSSSSSSSSSGGKRR 202  
DB 184 PVRITSRK---SSSSSSSSSSSTSSSEN--GKLKRR 214

## RESULT 2

US-09-533-029-18  
; Sequence 18, Application US/09533029  
; Patent No. 6664446  
; GENERAL INFORMATION:  
; APPLICANT: Heard, Jacqueline  
; APPLICANT: Brown, Pierre  
; APPLICANT: Kiechmann, Jose-Luis  
; APPLICANT: Kieddie, James  
; APPLICANT: Pineda, Omatra  
; APPLICANT: Adam, Luc  
; APPLICANT: Samaha, Raymond  
; APPLICANT: Zhang, James  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ratscliffe, Oliver  
; APPLICANT: Pilgrim, Marsha  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Reuber, Lynne  
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES  
; FILE REFERENCE: MB1-010  
; CURRENT APPLICATION NUMBER: US/09/533,029  
; CURRENT FILING DATE: 2000-03-22  
; EARLIER APPLICATION NUMBER: 60/125,814  
; EARLIER FILING DATE: 1999-03-23  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; OTHER INFORMATION: G28  
US-09-533-029-18

## Query Match

Best Local Similarity 30.6%; Score 324; DB 4; Length 268;  
Matches 91; Conservative 27; Mismatches 69; Indels 66; Gaps 9;

QY 1 MSEIISVSDRPLSLIIEHLSDN---SDSSSELTST----- 36  
DB 1 MSMTADSQSDYALFSLIRHLGSESEPISESTASVTOSCTGOSIKRYGRNPSFKL 60  
QY 37 -----BNW-----EIPADFL-----NW-----SGSEIQKRGSPS--SSCOSN 69  
DB 61 YPCFTSWGDLPLKENDSEMDLVYGLINDAFHGMWPESSSSDDEDRSPSVKIEPESF 120  
QY 70 SMAESQOEDSVGTPPEAAAGCGCKDMNRKGVRRPQKFAEIRDKKKSGRIWGT 129  
DB 121 AAVDSVPVKKKETSPPVSAATTAAGK--HYRGVRRPQKFAEIRDPKAGARWLG 177  
QY 130 YETPEDAALAYDAAAFNRGAKARLNFPHLIGSNISGVRVPRKRPAPETSTSSSS 189  
DB 178 FETAEADALAYDAAAFNRGSRALLNPLRVNSGEPDPVITSRK-----SSFS 226  
QY 190 SSENSSGGRKRR 202  
DB 227 SSNN--GAPKRR 238

## RESULT 3

US-09-202-161B-1  
; Sequence 1, Application US/09202161B  
; Patent No. 6653533  
; GENERAL INFORMATION:  
; APPLICANT: Purdue Research Foundation  
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS  
; FILE REFERENCE: 7024-371  
; CURRENT APPLICATION NUMBER: US/09/202,161B

; CURRENT FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: PCT/US97/10382  
; PRIOR FILING DATE: 1997-06-12  
; PRIOR APPLICATION NUMBER: 60/046,494  
; PRIOR FILING DATE: 1997-05-14  
; PRIOR APPLICATION NUMBER: 60/019,633  
; PRIOR FILING DATE: 1996-06-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: ASCII  
; SEQ ID NO 1  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Lycopersicon esculentum  
US-09-202-161B-1

## Query Match

Best Local Similarity 28.2%; Score 298.5; DB 4; Length 231;  
Matches 67; Conservative 18; Mismatches 50; Indels 19; Gaps 3;

QY 49 NWSGSEIQKRGSPSSSCQSNMAESQOEDSVGTPPEAAAGCGCKDMNRKGVRRP 108  
DB 65 NFTAQGVKSEPREIESSEPFSS-----PSPAGT---TAPAAETPKGRHRYGVQRW 114  
QY 109 GKFAEIRDPKKGSRWLTGTETPEDAALAYDAAAFNRGAKARLNFPHLIGSNISGV 168  
DB 115 GKFAEIRDPKAGARWLTGTETAEBAALAYDKAAYRRGSKXHLNPFHRIGLNPEPF 174  
QY 169 RVNPRKRPAPETSTSSSSSSSSSSSGGKRR 202  
DB 175 ELRRKRAIOGP-----ASSSGNSMKRR 199

## RESULT 4

US-08-912-272-18  
; Sequence 18, Application US/08912272  
; Patent No. 6093874  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamoto, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,272  
; FILING DATE: 15-AUG-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baebian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067220US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids

```

; APPLICANT: Finkelstein, Ruth R.
; APPLICANT: Lynch, Tim
; APPLICANT: Goodman, Howard M.
; APPLICANT: Wang, Ming-Li
; TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
; FILE REFERENCE: 480-89 (HV)
; CURRENT APPLICATION NUMBER: US/09/300,672
; CURRENT FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 60
; TYPE: PRT
; ORGANISM: AP2 domain protein
US-09-300-672-9

Query Match      25.1%; Score 266; DB 3; Length 60;
Best Local Similarity 78.0%; Pred. No. 6,7e-23;
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps

Cy          100 YKGVRRRPMWCKFAAEIRDPKKKGSRIMLGTGYTEPDEDAALAYDAAAFFNMGAKARILNFPH 158
             |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db           1 YRGVRRRPMWCKFAAEIRDPKXGARGRWLGTYETDEDAALAYDKAAVRMGSAHLNFPH 59

RESULT 7
US-09-202-161B-2
; Sequence 2, Application US/09202161B
; Patent No. 6653533
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-371
; CURRENT APPLICATION NUMBER: US/09/202,161B
; CURRENT FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: PCT/US97/10382
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/046,494
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PRIOR FILING DATE: 1997-05-14  
PRIOR APPLICATION NUMBER: 60/019,633  
PRIOR FILING DATE: 1996-06-12  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: ASCII  
SEQ ID NO 2  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Lycopersicon esculentum  
US-09-202-161B-2

Query Match 25.1%; Score 266; DB 4; Length 161;  
Best Local Similarity 55.6%; Pred. No. 3e-22;  
Matches 55; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

QY 99 RYGVRRRPMGKFAAIRDPKKKGRIMGTETPEDALAYDAAPFMNKGAKALNFP 158  
DB 58 KYGVRRRPMGKFAAIRDSARHGAHVWIGTETAEALAYDAAPFMNKGAKALNFP 117

QY 159 LIGSNISGVVPRKRPAPSPSTSSSSSSSSSSSG 197  
DB 118 EI---VNASVSD-KISLCSNSYTTNNSSLSNEVSSG 152

RESULT 8  
US-08-949-603-11  
Sequence 11, Application US/08949603  
Patent No. 5891859  
GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and  
APPLICANT: Eric J. Stockinger  
TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,603  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/706,270  
FILING DATE: September 4, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-384  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5891859e  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61  
TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:

ORIGINAL SOURCE:  
ORGANISM: Tobacco  
STRAIN:  
INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: N/A  
POSITION IN GENOME: N/A  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: sequencing  
OTHER INFORMATION: Figure 2D  
PUBLICATION INFORMATION:  
US-08-949-603-11

Query Match 24.8%; Score 262; DB 2; Length 61;  
Best Local Similarity 78.0%; Pred. No. 2e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRRPMGKFAAIRDPKKKGRIMGTETPEDALAYDAAPFMNKGAKALNFP 158  
DB 2 YRGVRRRPMGKFAAIRDPKNGARVWIGTETAEALAYDAAPFMNKGAKALNFP 60

RESULT 9  
US-08-706-270A-11  
Sequence 11, Application US/08706270A  
Patent No. 5892009  
GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and  
APPLICANT: Eric J. Stockinger  
TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,270A  
FILING DATE: September 4, 1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-310  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5892009e  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61  
TYPE: Amino Acid  
STRANDEDNESS: Single

TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Tobacco  
STRAIN:  
INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: N/A  
POSITION IN GENOME: N/A  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: sequencing  
OTHER INFORMATION: Figure 2D  
PUBLICATION INFORMATION:  
US-08-706-270A-11

Query Match 24.8%; Score 262; DB 2; Length 61;  
Best Local Similarity 78.0%; Pred. No. 2e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 100 YKGVRRPVGKFAEIRDPKKGSRIMLTGYPEPDALAYDAAFNMGAKARLNPPH 158  
Db 2 YKGVRRPVGKFAEIRDPKKGSRIMLTGYPEPDALAYDAAFNMGAKARLNPPH 60

RESULT 10  
US-08-949-580-11  
Sequence 11, Application US/08949580  
Patent No. 5929305  
GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and  
APPLICANT: Eric J. Stockinger  
TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
NUMBER OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,580  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/706,270  
FILING DATE: September 4, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5929305e

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61  
TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Tobacco  
STRAIN:  
INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: N/A  
POSITION IN GENOME: N/A  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: sequencing  
OTHER INFORMATION: Figure 2D  
PUBLICATION INFORMATION:  
US-08-949-580-11

Query Match 24.8%; Score 262; DB 2; Length 61;  
Best Local Similarity 78.0%; Pred. No. 2e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 100 YKGVRRPVGKFAEIRDPKKGSRIMLTGYPEPDALAYDAAFNMGAKARLNPPH 158  
Db 2 YKGVRRPVGKFAEIRDPKKGSRIMLTGYPEPDALAYDAAFNMGAKARLNPPH 60

RESULT 11  
US-08-950-172A-11  
Sequence 11, Application US/08950172A  
Patent No. 5965705  
GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and  
APPLICANT: Eric J. Stockinger  
TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
NUMBER OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/950,172A  
FILING DATE: 10/14/1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/949,580  
FILING DATE: October 14, 1997  
APPLICATION NUMBER: 08/706,270  
FILING DATE: September 4, 1996  
ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION NUMBER: US 09/018,227  
PRIOR FILING DATE: 1998-02-03

US-09-601-802D-134  
; Sequence 134, Application US/09601802L  
: Patent No 6706866

; Patent No. 6706866  
; GENERAL INFORMATION:



APPLICANT: Thomashow, Michael  
APPLICANT: Stockinger, Eric  
APPLICANT: Jaglo-Otosen, Kirsten  
APPLICANT: Gilmour, Sarah  
APPLICANT: Zaika, Daniel  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Zhang, James  
APPLICANT: Haake, Volker  
TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL  
STRESS TOLERANCE  
FILE REFERENCE: 51442000201/MB10029  
CURRENT APPLICATION NUMBER: US/09/601,802D  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/018,233  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/017,816  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/018,235  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/017,575  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/018,227  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/018,234  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/198,119  
PRIOR FILING DATE: 1998-11-23  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 134  
LENGTH: 63  
TYPE: PRT  
ORGANISM: Nicotiana tabacum  
US-09-601-802D-134

Query Match 24.8%; Score 262; DB 4; Length 63;  
Best Local Similarity 78.0%; Pred. No. 2,1e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPVGKFAEIRDPKKGSRWLGYETPEDAALAYDAAAFNRGAKARLNP 158  
DB 4 YRGVRRPVGKFAEIRDPKKGSRWLGYETPEDAALAYDAAAFNRGAKARLNP 62

US-08-912-272-17  
Sequence 17, Application US/08912272  
Patent No. 6093874  
GENERAL INFORMATION:  
APPLICANT: Jofuku, K. Diane  
APPLICANT: Okamoto, Jack K.  
TITLE OF INVENTION: Methods for Improving Seeds  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,272  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/879,827  
FILING DATE: 20-JUN-1997  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/700,152  
FILING DATE: 20-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Baselian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-067220US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..69  
OTHER INFORMATION: /note="AP2 domain within tobacco  
EREBP-1"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 36..51  
OTHER INFORMATION: /note="putative EREBP-1 amphipathic  
alpha-helix"  
US-08-912-272-17

Query Match 24.4%; Score 258; DB 3; Length 69;  
Best Local Similarity 77.6%; Pred. No. 6,9e-22;  
Matches 45; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPVGKFAEIRDPKKGSRWLGYETPEDAALAYDAAAFNRGAKARLNP 157  
DB 4 YRGVRRPVGKFAEIRDPKKGSRWLGYETPEDAALAYDAAAFNRGAKARLNP 61

Search completed: February 27, 2005, 22:07:39  
Job time: 44 secs

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Db 181 STSSSSSSSSSSSGRRKRRY 203
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RESULT 2
ID 08L9R3 PRELIMINARY; PRT; 202 AA.
AC 08L9R3;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Ethylene-responsive element binding protein 1.
GN Name=EREBP1;
OS Glycine max (Soybean);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22054140; PubMed=12059106;
RA Mazarei M., Puthoff D.P., Hart J.K., Rodermel S.R., Baum T.J.;
RT "Identification and characterization of a soybean ethylene-responsive
RT element binding protein gene whose mRNA expression changes during
RT soybean cyst nematode infection.";
RL Mol. Plant Microbe Interact. 15:577-586(2002).
DR EMBL; AF537211; AAM45475.1; -
DR HSSP; 080337; 2GCG.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001471; TF_ERF.
DR PRINTS; PR00367; ETHRSPLEMT.
DR PRODOM; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ SEQUENCE 202 AA; 22467 MW; 1B875ACEB2A7D56D CRC64;

Query Match 9.4%; Score 19; DB 2; Length 202;
Best Local Similarity 100.0%; Pred.No.1.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 102 GVRRRPWGKFAAETRDPKK 120
|||||
Db 79 GVRRRPWGKFAAETRDPKK 97

RESULT 3
ID 022167 PRELIMINARY; PRT; 226 AA.
AC 022167;
DT 01-JUN-1998 (TEMBLrel. 05, Created)
DT 01-JUN-1998 (TEMBLrel. 05, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Putative ethylene response element binding protein (Putative ethylene
DE response element binding protein; EREBP).
GN Name=At2g44440;
OS Arabidopsis thaliana (Mouse-ear cress);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Rounleay S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Skyes S.M., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
RA Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
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RN [3]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh U., Carlini P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shin P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Theologis A., Ecker J., Davis R.W.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh U., Carlini P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shin P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002388; AAC31840.1; -
DR EMBL; AY072471; AAL66886.1; -
DR EMBL; AF325089; AAK17157.1; -
DR EMBL; AF370540; AAK48967.1; -
DR PIR; T00409; T00409.
DR HSSP; 080337; 2GCG.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001471; TF_ERF.
DR PRINTS; PR00367; ETHRSPLEMT.
DR PRODOM; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ SEQUENCE 226 AA; 25353 MW; 4B2EF81CDD856987 CRC64;

Query Match 9.4%; Score 19; DB 2; Length 226;
Best Local Similarity 100.0%; Pred.No.2.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 102 GVRRRPWGKFAAETRDPKK 120
|||||
Db 94 GVRRRPWGKFAAETRDPKK 112

RESULT 4
ID 08L9K1 PRELIMINARY; PRT; 226 AA.
AC 08L9K1;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Putative ethylene response element binding protein (EREBP).
GN Arabidopsis thaliana (Mouse-ear cress);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RL "Full-length messenger RNA sequences greatly improve genome
RL annotation.";
RN [2]
RP SEQUENCE FROM N.A.
RX Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
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RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY088387; AAM65925.1; -.
DR HSSP; 080337; 2GCC.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001471; TF_ERF.
DR PRINTS; PR00367; ETHRSP_ELMNT.
DR ProDom; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
DR POSITIVE; PS00697; DNA_LIGASE_A1; UNKNOWN; 1.
SQ SEQUENCE 226 AA; 25367 MW; C3F80438CF19D80 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPWGKFAAIRDPK 120
Db 94 GVRRRPWGKFAAIRDPK 112

RESULT 5
O9LEM6 PRELIMINARY; PRT; 210 AA.
AC O9LEM6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE AP2-domain DNA-binding protein.
GN Name=orca2;
OS Catharanthus roseus (rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vincaceae;
OC Catharanthus.
OC NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gdon; TISSUE=Cell suspension;
RX MEDLINE=99380162; Pubmed=10449411; DOI=10.1093/emboj/18.16.4455;
RA Menke F.L.H., Champion A., Kijne J.W., Memelink J.;
RT "A novel jasmonate- and elicitor-responsive element in the periwinkle
RT secondary metabolite biosynthetic gene Str interacts with a jasmonate-
RT and elicitor-inducible AP2-domain transcription factor, ORCA2."
RL EMBO J. 18:4455-4463(1999).
DR EMBL; AJ238740; CAB93940.1; -.
DR HSSP; 080337; 2GCC.
DR TRANSFAC; T04749; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001471; TF_ERF.
DR PRINTS; PR00367; ETHRSP_ELMNT.
DR ProDom; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
DR DNA-binding.
SQ SEQUENCE 210 AA; 24021 MW; 017DF088F713CE38 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPWGKFAAIRDPK 119
Db 129 GVRRRPWGKFAAIRDPK 146

RESULT 6
O7XDZ2 PRELIMINARY; PRT; 124 AA.
ID O7XDZ2

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AC O7XDZ2;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Putative retrovirus-related pol polyprotein from transposon TNT.
GN ORFNames=OSJNBa0094K20.5;
OS Oryza sativa (Japanese cultivated rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "in-depth view of structure, activity, and evolution of rice
RT chromosome 10."
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017099; AAP5399.1; -.
DR HSSP; 080337; 1GCC.
DR Gramene; O7XDZ2; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001471; TF_ERF.
DR ProDom; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
DR Polyprotein.
SQ SEQUENCE 124 AA; 13306 MW; CB857D9A551D81BE CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 9.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPWGKFAAIRDP 118
Db 15 GVRRRPWGKFAAIRDP 31

RESULT 7
O6MWK9 PRELIMINARY; PRT; 128 AA.
AC O6MWK9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE B1234D02.6 protein.
GN Name=B1234D02.6;
OS Oryza sativa (Japanese cultivated rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX Pubmed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu X., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Mu Y., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Han U., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RL "Sequence and analysis of rice chromosome 4."
RN [2]
RP Nature 420:316-320(2002).
SQ SEQUENCE FROM N.A.

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RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,  
 RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,  
 RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,  
 RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,  
 RA Hao P., Zhang L., Mu M., Zhang R.O., Guan J.P., Fu G., Wang S.Y.,  
 RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,  
 RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,  
 RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,  
 RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.P.,  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BX842602; CA75882.1; -;  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR Pfam: PF00847; AP2; 1.  
 DR PRINTS: PR00367; ETHRSPELEMT.  
 DR ProDom: PD001423; TF\_ERF; 1.  
 DR SMART: SM00380; AP2; 1.  
 SQ SEQUENCE 128 AA; 14193 MW; 3BABAFPA81210A6 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAEIRDP 118  
 Db 14 GVRRRPWGKFAEIRDP 30

RESULT 8  
 ID 09LTC5 PRELIMINARY; PRT; 139 AA.  
 AC 09LTC5;  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Nicotiana glauca 3-like protein (Putative ethylene responsive element  
 DE binding protein).

OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
 RT clones".  
 RL DNA Res. 7:131-135(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.

RA Gong W., Pan Y., Peng X.Y., Yang J., Zhu Y.X.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB025608; BA95736.1; -;  
 DR EMBL: AF580377; CA645639.1; -;  
 DR HSSP: O80337; ZGCC.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS: PR00367; ETHRSPELEMT.  
 DR ProDom: PD001423; TF\_ERF; 1.  
 SQ SEQUENCE 139 AA; 16096 MW; 5E43AB05E93B4050 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 102 GVRRRPWGKFAEIRDP 118  
 Db 22 GVRRRPWGKFAEIRDP 38

RESULT 9  
 ID 075U5 PRELIMINARY; PRT; 165 AA.  
 AC 075U5;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE ERF-like protein.  
 GN Name=CME-ERF;  
 OS Cucumis melo (Muskmelon).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
 OC NCBI\_TaxID=3656;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Minano S., Sato T.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB125975; BAD0155.1; -;  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR Pfam: PF00847; AP2; 1.  
 DR PRINTS: PR00367; ETHRSPELEMT.  
 DR ProDom: PD001423; TF\_ERF; 1.  
 DR SMART: SM00380; AP2; 1.  
 SQ SEQUENCE 165 AA; 19063 MW; 0A829B3A53E0ADB9 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAEIRDP 118  
 Db 85 GVRRRPWGKFAEIRDP 101

RESULT 10  
 ID 08IDL4 PRELIMINARY; PRT; 201 AA.  
 AC 08IDL4;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Ethylene responsive element binding factor-like.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22088475; PubMed=12093376;  
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
 RL "Full-length messenger RNA sequences greatly improve genome  
 RL annotation." J. RESEARCH 10029-RESEARCH10029 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.,  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY085939; AAM63150.1; -;  
 DR HSSP: O80337; ZGCC.

DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SO SEQUENCE 201 AA; 22780 MW; 63511AF9BFBF0404 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
 DB 109 GVRRRPWGKFAAEIRDP 125

RESULT 11  
 084XB0  
 ID 084XB0 PRELIMINARY; PRT; 201 AA.  
 AC 084XB0;  
 DT 01-JUN-2003 (TReMBLrel. 24, Created)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Ethylene response factor 4.  
 GN Name=ERF4;  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 NC NCB1\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22816770; PubMed=12935902; DOI=10.1016/S0014-5793(03)00757-9;  
 RA Tournebise B., Sanchez-Ballesteria M.T., Jones B., Pesquet E., Regad F.,  
 RA Latche A., Béch J.C., Bouzayen M.;  
 RT "New members of the tomato ERF family show specific expression pattern  
 and diverse DNA-binding capacity to the GCC box element.";  
 RL FEBS Lett. 550:149-154(2003).  
 DR EMBL; AY192370; AA034706.1; -.  
 DR HSSP; O80337; 2GCC.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SO SEQUENCE 201 AA; 22599 MW; 76075F3710881C90 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
 DB 121 GVRRRPWGKFAAEIRDP 137

RESULT 12  
 09FKG2  
 ID 09FKG2 PRELIMINARY; PRT; 201 AA.  
 AC 09FKG2;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Transcription factor-like protein (putative ethylene responsive  
 element binding factor).  
 GN Name=At5G61590;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCB1\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98403884; PubMed=9734815;  
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
 RT Sequence features of the regions of 1,367,185 bp covered by 19  
 RT physically assigned P1 and P1C clones.";  
 RL DNA Res. 5:203-216(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,  
 RA Carinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
 RA Seki M., Shim P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,  
 RA Toriumi M., Yu G., Brooks S., Chao O., Chen H., Karlin-Neumann G.,  
 RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,  
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB012239; BAB09003.1; -.  
 DR EMBL; AY045968; AAK76642.1; -.  
 DR EMBL; AY079321; AAL85052.1; -.  
 DR HSSP; O80337; 2GCC.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SO SEQUENCE 201 AA; 22727 MW; 09BF68FB81696 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
 DB 109 GVRRRPWGKFAAEIRDP 125

RESULT 13  
 06V5F2  
 ID 06V5F2 PRELIMINARY; PRT; 204 AA.  
 AC 06V5F2;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE AP2 transcription factor.  
 GN CRFNames=Cr 7580;  
 OS Capsella rubella.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Capsella.  
 NC NCB1\_TaxID=81985;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SRRAIN=Circus maximus;  
 RX PubMed=14970339; DOI=10.1073/pnas.0305448101;  
 RA Flehig A., Kilmport R., Preuss D.;  
 RT "Comparisons of pollen coat genes across Brassicaceae species reveal  
 RT rapid evolution by repeat expansion and diversification.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:3286-3291(2004).  
 DR EMBL; AY350713; AAR15465.1; -.

DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR Pfam; PF00847; AP2; 1.  
 DR PRINTS; PR00367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SQ SEQUENCE 204 AA; 23008 MW; E1D965603C9A4DCB CRC64;

Query Match 8.4%; Score 17; DB 2; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPWGKFAAEIRDP 118  
 |||||  
 Db 109 GVRRRPWGKFAAEIRDP 125

RESULT 14  
 Q6V5J8

ID Q6V5J8 PRELIMINARY; PRT; 206 AA.

AC Q6V5J8;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DE AP2 transcription factor/ethylene response element.  
 GN ORFNames=Bo\_7580;  
 OS Brassica oleracea (Cauliflower).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurooids II; Brassicales; Brassicaceae; Brassica.  
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 RC STRAIN=A12DRD;  
 RX PubMed=14970339; DOI=10.1073/pnas.0305448101;  
 RA Flehig A., Kimport R., Preuss D.;  
 RT "Comparisons of pollen coat genes across Brassicaceae species reveal  
 RT rapid evolution by repeat expansion and diversification";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:3286-3291(2004).  
 DR EMBL; AY350710; ARI13699.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR Pfam; PF00847; AP2; 1.  
 DR PRINTS; PR00367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPWGKFAAEIRDP 118  
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RESULT 15

ID Q6V5B8 PRELIMINARY; PRT; 207 AA.

AC Q6V5B8;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
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 GN ORFNames=Aal\_7580;  
 OS Arabidopsis arenosa.  
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OC eurooids II; Brassicales; Brassicaceae; Arabidopsis.  
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 RC STRAIN=care-1;  
 RX PubMed=14970339; DOI=10.1073/pnas.0305448101;  
 RA Flehig A., Kimport R., Preuss D.;  
 RT "Comparisons of pollen coat genes across Brassicaceae species reveal  
 RT rapid evolution by repeat expansion and diversification";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:3286-3291(2004).  
 DR EMBL; AY350715; ARI15499.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:transcription factor activity; IEA.  
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 Db 112 GVRRRPWGKFAAEIRDP 128

Search completed: February 27, 2005, 22:26:24  
 Job time : 176 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 15:41:26 ; Search time 3857 Seconds  
(without alignments)  
9949.840 Million cell updates/sec

Title: US-09-890-782-3

Perfect score: 1 ttcttaaaaaagaagaataat.....ttatattcccaaaaagttcac 792

Sequence:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hng:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_str:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	100.0	792	6	BD269586 Method of
2	792	100.0	792	6	AX033192 Sequence
3	792	100.0	825	8	CRO251249 Catharant
4	792	100.0	1816	6	CRO251250 Catharant
5	155.2	19.6	924	6	CO808982 Sequence
6	135.6	17.1	914	8	AY088387 Arabidops
7	134	16.9	681	6	CO805290 Sequence
8	134	16.9	681	6	AX507520 Sequence
9	134	16.9	681	6	AF325089 Arabidops
10	134	16.9	727	8	AF325089 Arabidops
11	134	16.9	841	8	TOBRY4A Arabidops
12	134	16.9	887	8	AF370540 Arabidops
13	134	16.9	85534	8	AC002388 Arabidops
14	132.6	16.7	885	6	BD269585 Sequence
15	132.6	16.7	885	6	AX033191 Sequence
16	132.6	16.7	905	8	CRO28740 Catharant
17	131.4	16.6	703	8	AF057373 Nicotiana
18	129.8	16.4	704	8	LEU89255 Lycopersico
19	129.4	16.3	708	6	BD248325 Tobacco-o

20	125	15.8	76730	8	AP004533 Lycopersi
21	123.8	15.6	939	8	BT013151 Lycopersi
22	122.2	15.4	931	8	AY192367 Lycopersi
23	121.4	15.3	947	8	TOBRY4D Arabidops
24	117	14.8	858	6	CO808845 Sequence
25	116.2	14.7	933	6	BD194702 Genes enh
26	116.2	14.7	933	6	AR432951 Sequence
27	113.6	14.3	761	8	AF357211 Glycine m
28	112.2	14.2	963	8	AY086983 Arabidops
29	111.2	14.0	3688	8	AB016264 Nicotiana
30	110.6	14.0	732	6	AX412264 Sequence
31	110.6	14.0	732	6	AX412265 Sequence
32	110.6	14.0	732	6	AX412465 Sequence
33	110.6	14.0	732	6	AX412559 Sequence
34	110.6	14.0	732	6	AX412895 Sequence
35	110.6	14.0	732	6	AX505459 Sequence
36	110.6	14.0	732	6	AX651319 Sequence
37	110.6	14.0	908	8	AK175151 Arabidops
38	110.6	14.0	913	6	AR439817 Sequence
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#### ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Method of modulating biosynthesis of metabolite in recombinant somatic cells.  
ACCESSION BD269586.1 GI:33079354  
VERSION JP 2002535993-A/3.  
KEYWORDS Catharanthus roseus (Madagascar periwinkle)  
SOURCE Catharanthus roseus  
ORGANISM Catharanthus roseus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Gentianales; Apocynaceae; Rauvolfiaceae; Vincet; Catharanthus.  
1 (bases 1 to 792)  
Memelink,J., Der,C.T.E.V., Fits, Menke,F.L.H. and Kijne,J.W.  
Method of modulating biosynthesis of metabolite in recombinant somatic cells  
Patent: JP 2002535993-A 3 29-OCT-2002;  
RUKSUNIVERSITEIT LEIDEN  
OS Catharanthus roseus (madagascar periwinkle)  
PN JP 2002535993-A/3  
PD 29-OCT-2002  
PP 07-FEB-2000 JP 2000597442  
PR 05-FEB-1999 DK PA 199900158,10-FEB-1999 US 60/119388 PI  
JOHAN MEMELINK, CORNELIA THEODORA ELISABETH VAN DER FITS, PI  
FRANCISCUS LEONARDUS HENDRIKUS MENKE, JAN WILLEM KIJNE PC  
C12N15/09,A01H5/00,C12N5/10,C12P5/00,C12P7/22,C12P13/00,C12P17/ PC  
10, C12N15/00,C12N5/00  
PC Method of modulating biosynthesis of metabolite in recombinant somatic cells  
CC  
CC cells  
CC Key  
FH Key  
FH source  
FT source

FEATURES  
source  
Location/Qualifiers  
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/organism="Catharanthus roseus"  
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## ORIGIN

/db\_xref="taxon:4058"

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 Best Local Similarity 100.0%; Pred. No. 1.1e-205;  
 Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ACCESSION AX033192  
 VERSION AX033192.1 GI:10280047  
 KEYWORDS  
 SOURCE Catharanthus roseus (Madagascar periwinkle)  
 ORGANISM Catharanthus roseus

## REFERENCE

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamiales; Gentianales; Apocynaceae; Rauvolfioideae;  
 Vincaceae; Catharanthus.

## JOURNAL

Memelink, J., Kijne, J.W., Menke, F.L. and van der Pijl, C.T.  
 Method of modulating metabolite biosynthesis in recombinant cells  
 Patent: WO 0046383-A 3 10-AUG-2000;  
 UNIV LEIDEN (NL); MEMELINK JOHAN (NL); FITS CORNELIA THEODORA  
 ELISABE (NL); KIJNE JAN WILLEM (NL); MENKE FRANK LEONARDUS  
 HENDRIKU (NL)

## FEATURES

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## ORIGIN

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 DB 1 TTTTAAAAAGAGAAAAATGTCGGAAGATCATTTCCGTCAGATGATTTCTTCTT 60  
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 Db 781 AAAAAGTTCAC 792

RESULT 3  
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 LOCUS Catharanthus roseus mRNA for AP2-domain DNA-binding protein (orca3 gene).  
 DEFINITION  
 ACCESSION AJ251249  
 VERSION AJ251249.1 GI:8980312  
 KEYWORDS AP2-domain DNA-binding protein; orca3 gene.  
 SOURCE Catharanthus roseus (Madagascar periwinkle)  
 ORGANISM Catharanthus roseus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae; Catharanthus.

REFERENCE 1  
 AUTHORS van der Fits, L. and Memelink, J.  
 TITLE ORCA3, a jasmonate-responsive transcriptional regulator of plant primary and secondary metabolism  
 JOURNAL Science 289 (5477), 295-297 (2000)  
 MEDLINE 20355201  
 PUBMED 10894776  
 REFERENCE 2 (bases 1 to 825)  
 AUTHORS Memelink, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-NOV-1999) Memelink J., Institute of Molecular Plant Sciences, Leiden University, Wassenaarseweg 64, NL-2333 AL, NETHERLANDS

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QY 781 AAAAAGTTCAC 792  
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RESULT 4  
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 DEFINITION  
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 VERSION AJ251250.1 GI:8980314  
 KEYWORDS AP2-domain DNA-binding protein; orca3 gene.  
 SOURCE Catharanthus roseus (Madagascar periwinkle)  
 ORGANISM Catharanthus roseus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae; Catharanthus.

REFERENCE 1  
 AUTHORS van der Fits, L. and Memelink, J.  
 TITLE ORCA3, a jasmonate-responsive transcriptional regulator of plant primary and secondary metabolism  
 JOURNAL Science 289 (5477), 295-297 (2000)  
 MEDLINE 20355201  
 PUBMED 10894776  
 REFERENCE 2 (bases 1 to 1816)  
 AUTHORS Memelink, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-NOV-1999) Memelink J., Institute of Molecular Plant Sciences, Leiden University, Wassenaarseweg 64, NL-2333 AL,



LOCUS	AY088387	914 bp	mRNA	linear	PLN 14-APR-2003
DEFINITION	Arabidopsis thaliana clone 6337	mRNA, complete sequence.			
ACCESSION	AY088387				
VERSION	AY088387.1	GI:21407161			
KEYWORDS	FLI CDNA.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 914)				
AUTHORS	Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.				
TITLE	Full-length messenger RNA sequences greatly improve genome annotation				
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)				
MEDLINE	22088475				
PUBMED	12093376				
REFERENCE	2 (bases 1 to 914)				
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.				
TITLE	Full-length cDNA from Arabidopsis thaliana				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 914)				
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA				
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.				
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	CSYEDNR"				
ORIGIN					
	Query Match	17.1%;	Score 135.6;	DB 8;	Length 914;
	Best Local Similarity	64.2%;	Pred. NO. 7.6e-26;		
	Matches 204;	Conservative 0;	Mismatches 114;	Indels 0;	Gaps 0;
DB	233 CGAAGAGTCGACAGAGATTCTGTTGGGAAACCCCGCCAGAACCGCGCCGAGAG 292				
	230 CCGTACTCTCTCCGGCGGAGAAATGAAGCTTCGCGGACGAAAGCGAGTGGCTCACA 349				

OY		293	GTTGTTCCAAAGATTGGAAACCGGTATTAAGGCCCTTAAACGGCAGCCGTCGGGGGAAATTGC	352
Dd		350	CGCCGAGCGCAAGAAGGGGATGCAATGACAGAGAGTGAGGAGAGAGCCCTGGGGGAAATTTCG	409
OY		353	CGGCGGAGATTAAGGGATCCGAAAAAAGAAAGANTCCAGGATTTGGTTGGGTATCATACGGA	412
Dd		410	CGGCGGAGATTAGGGATTCGAAAGAAAGAACGAGCTTAGGGTTTGGCTCGGACTTACGAGA	469
OY		413	CACCTGAGGATGCAGCATTTGGCTTATGATGCAGCCGCTTTAATAATATGCGTGGAGCTAAG	472
Dd		470	CGCCGAGAGACCGCGCGGTGCGTACGACCAGCGGCGCTTTACAGCTCACAGAGANTGAAAG	529
OY		473	CTAGGCTTAATTTTTCTCATTTGATTTGGTTGGATTAATTTCCGAGCCGTTAGAGTAAC	532
Dd		530	CTAAGCTGAATTTTCCGATTTGATTTGATTTGTTCTTGTAGTATGAGCCGCTTAGATTAGGC	589
OY		533	CGAGAAAACGTTTCCTG	550
Dd		590	CTGCGCCGTCGCTCGCCG	607
RESULT 7				
LOCUS	CQ805290	681 bp	DNA	linear PAT 10-MAY-2004
DEFINITION	Sequence 1701 from Patent WO2004035798.			
ACCESSION	CQ805290			
VERSION	CQ805290.1 GI:47111279			
KEYWORDS				
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroside II; Brassicales; Brassicaceae; Arabidopsiis.			
REFERENCE	1 Inze,D., de Veylder,L. and Vlieghe,K. Identification of novel e2f target genes and use thereof Patent: WO 2004035798-A 1701 29-APR-2004;			
AUTHORS	CropDesign N.V. (BR)			
TITLE	Location/Qualifiers			
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	Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;			
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Dd		251	CGCCGAGSGCAAGAGGATGCAATGACAGAGAGTGAAGAGAGAGCCGTCGGGGGAAATTTCG	310
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Dd		311	CGGCGGAGATTAGGGATTCGAAAGAAAGAACGAGCTTAGGGTTTGGCTCGGACTTACGGA	370
OY		413	CACCTGAGGATGCAGCATTTGGCTTATGATGCAGCCGCGCTTTAATAATATGCGTGGAGCTAAG	472
Dd		371	CGCCGAGAGACCGCGCGGTGCGTACGACCAGCGCGCTTTACAGCTCACAGAGANTGAAAG	430
OY		473	CTAGGCTTAATTTTCTCATTTGATTTGGTTGGATTAATTTCCGAGCCGTTAGAGTAAC	532
Dd		431	CTAAGCTGAATTTTCCGATTTGATTTGATTTGTTCTTGTAGTATGAGCCGCTTAGATTAGGC	490
OY		533	CGAGAAAACGTTTCCTG	550
Dd		491	CTGCGCCGTCGCTCGCCG	508

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 ACCESSION AX507520  
 VERSION AX507520.1 GI:23388757  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana (thale cress)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE  
 1 Harper, J.F., Kreps, J., Wang, X. and Zhu, T.  
 Stress-regulated genes of plants, transgenic plants containing same, and methods of use  
 Patent: WO 0216655-A 2215 28-FEB-2002;  
 The Scripps Research Institute (US); Syngenta Participations AG (CH)

FEATURES  
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 Query Match 16.9%; Score 134; DB 6; Length 681;  
 Best Local Similarity 63.8%; Pred. No. 2e-25;  
 Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

233 CGGAAAGCTGTGACGAGATTCTGTGTGGGAAACCCCGCAGAAAGCGCGCGGAGAG 292  
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RESULT 9  
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 LOCUS AF325089  
 DEFINITION Arabidopsis thaliana putative ethylene response element binding protein (EREBP) (At2g44840) mRNA, complete cds.  
 ACCESSION AF325089  
 VERSION AF325089.1 GI:13372436  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana (thale cress)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE  
 1 (bases 1 to 681)  
 Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C.J., Theologis, A., Ecker, J. and Davis, R.W.  
 Direct Submission

JOURNAL  
 Submitted (30-NOV-2000) DNA Sequencing and Technology Center,  
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
 USA

FEATURES  
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 Location/Qualifiers  
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ORIGIN  
 Query Match 16.9%; Score 134; DB 8; Length 681;  
 Best Local Similarity 63.8%; Pred. No. 2e-25;  
 Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

233 CGGAAAGCTGTGACGAGATTCTGTGTGGGAAACCCCGCAGAAAGCGCGCGGAGAG 292  
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 431 CTAGGCTGAATTTTCCGCAATTTGATGTTGTTGAATGATGACCGGTTAGATTAGGC 490  
 533 CGAGAAACGTTTCCCTG 550  
 491 CTGCGCGTCCGCTCGCGG 508

RESULT 10  
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 LOCUS AY072471  
 DEFINITION Arabidopsis thaliana putative ethylene response element binding protein (EREBP) (At2g44840; T13F15.15) mRNA, complete cds.  
 ACCESSION AY072471  
 VERSION AY072471.1 GI:18377439  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana (thale cress)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE  
 1 (bases 1 to 727)  
 Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M., Palm, C.J., Bower, L., Jones, T., Bah, J., Carrinci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Nam, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shim, P., Yamada, K.,

TITLE  
JOURNAL

Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.  
Direct Submission  
Submitted (02-JAN-2002) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

COMMENT  
e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,  
Saton, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the  
sequencing and annotation of the RAFL cDNAs: Nguyen, M.,  
Soutwicz, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C. J.,  
Bower, L., Jones, J., Banb, J., Chen, H., Cheuk, R., Chung, M. K.,  
Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H., Shim, P.,  
Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.

Nguyen, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed  
equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.  
(SSP/Stanford) contributed equally to this work as PIs.

FEATURES  
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ORIGIN

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Db 491 CTCGCCGTCGCTCGCCG 508

RESULT 11

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LOCUS  
DEFINITION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum mRNA for ERF1, complete cds.  
D38123.1 GI:790359  
ERF1, ethylene-responsive transcription factor.  
Nicotiana tabacum (common tobacco)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanales; Solanales; Solanales;  
1 (bases 1 to 841)  
Ohme-Takagi, M. and Shinozaki, H.  
Ethylene-inducible DNA binding proteins that interact with an  
ethylene-responsive element  
Plant Cell 7 (2), 173-182 (1995)  
MEDLINE  
55276459  
7756828

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
55276459  
7756828

2 (sites)  
Suzuki, K., Suzuki, N., Ohme-Takagi, M. and Shinozaki, H.  
Immediate early induction of mRNAs for ethylene-responsive  
transcription factors in tobacco leaf strips after cutting  
Plant J. 15, 657-665 (1998)

Ohme-Takagi, M.  
Direct Submission  
Submitted (01-SEP-1994) Masaru Ohme-Takagi, National Institute of  
Bioscience and Human Technology, Plant Molecular Biology  
Laboratory, 1-1 Higashi, Tsukuba, Ibaraki 305, Japan  
(E-mail:masaru@nibh.go.jp, Tel:0298-54-6071, Fax:0298-54-6095)  
Sequence updated (04-Apr-1995) by:  
Masaru Ohme-Takagi.

COMMENT

FEATURES

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CDS

3'UTR  
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Query Match 16.9%; Score 134; DB 8; Length 841;  
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Qy 468 TAAAGTAGGCTTAATTTCCATTTGATGATTTGATTTCCGACCGGCTAGAGT 527

Db 494 AAGGCTCATTTAAATTTCCATATGAAATCGTTAAATGAAACGGAACCGGCTGAGT 553

Qy 528 AAACCCGAGAAACGTTTCCTGCGAGCGCTTCAAGACGTCGCTCTTCTTCTTC 587

Db 554 TAGCGGAAAGACGAGCATCCGCTGACCGGCTAGTTCGGAATAAGTCACTAA 613

Qy 588 TTGCTGAAATATGAGAGAAAGAA 617

Db 614 ACGGAGAGAAAGCTGTTGCAACTGAGAA 643

RESULT 12

AF370540 887 bp mRNA linear PLN 01-MAY-2001

LOCUS Arabidopsis thaliana putative ethylene response element binding

DEFINITION protein; ERBP (At2g44840; T13E15.15) mRNA, complete cds.

ACCESSION AF370540

VERSION AF370540.1 GI:13899090

KEYWORDS FULL CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 887)

AUTHORS Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Palm,C.D., Bower,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Marusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shimizu,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

TITLE Direct Submission

JOURNAL Submitted (17-APR-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT e-mail for correspondence: arab@sequence.stanford.edu

FEATURES

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ORIGIN

Query Match 16.9%; Score 134; DB 8; Length 887;

Best Local Similarity 63.8%; Pred. No. 2.1e-25;

Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 233 CGGAAAGCTGTCAAGAGATTCTGTGTGGAAACCCGCGCAGAAAGCGCGCGAGAG 292

Db 290 CCGTTACCTCTCCGCGGAGAAATAAGCTCCGCGACGAAGCGAGTGTCAAG 349

Qy 293 GTTGTGAAAGATTGGAACCGGTATPAGGCGCTTGAACGCGCGCGTGGGGAAGTTG 352

Db 350 CGCGGAGCAGAAAGGAGTCACTACAGAGATGAGAGAGCGCGTGGGGAATTCG 409

Qy 353 CGCGGAGATPAGGATCCGAAAAAGAAAGATCCAGATTTGGTTGGTACATACGAA 412

Db 410 CGCGGAGATPAGGATCCGAAAAAGAAAGATCCAGATTTGGTTGGTACATACGAA 469

Qy 413 CACCTGAGATGAGCATTTGCTTATGATGACCGCGCTTAAATATGCGTGAAG 472

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Qy 473 CTAGGCTTAATTTCTCATTTGTTGTTGCAATATTTCCGACCCGTTAGATAAC 532

Db 530 CTAGGCTTAATTTCTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 589

Qy 533 CGAGAAAGCTTTCCCTG 550

Db 590 CTCGCGCTCGCTCGCGG 607

RESULT 13

AC002388/c 85534 bp DNA linear PLN 11-MAR-2002

LOCUS Arabidopsis thaliana chromosome 2 clone T13E15 map m336, complete

DEFINITION sequence.

ACCESSION AC002388

VERSION AC002388.3 GI:20196917

KEYWORDS HTG.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 85534)

AUTHORS Rounsley,S.D., Lin,X., Ketchum,K.A., Crosby,M.L., Brandon,R.C., Sykes,S.M., Mason,T.M., Kerlavage,A.R., Adams,M.D., Somerville,C.R. and Venter,J.C.

TITLE Unpublished

JOURNAL 2 (bases 1 to 85534)

REFERENCE Lin,X.

AUTHORS Direct Submission

JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712

TITLE Medical Center Dr., Rockville, MD 20850, USA

REFERENCE 3 (bases 1 to 85534)

AUTHORS Town,C.D. and Kaul,S.

TITLE Direct Submission

JOURNAL Submitted (27-FEB-2002) The Institute for Genomic Research, 9712



Medical Center Dr, Rockville, MD 20850, USA, cdctown@igr.org  
On Apr 18, 2002 this sequence version replaced gi:6598367.  
COMMENT  
FEATURES  
source location/Qualifiers

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UNIV LEIDEN (NL) ; MEMELINK JOHAN (NL) ; FITS CORNELIA THEODORA  
ELISABE (NL) ; KIJNE JAN WILLEM (NL) ; MENKE FRANK LEONARDUS  
HENDRIKU (NL)

## FEATURES

Source

Location/Qualifiers

1..885

/organism="Catharanthus roseus"

/mol\_type="unassigned DNA"

/db\_xref="taxon:4058"

## ORIGIN

## Query Match

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Best Local Similarity 74.5% ; Pred. No. 5e-25 ;

Matches 181 ; Conservative 0 ; Mismatches 59 ; Indels 3 ; Gaps 1 ;

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Job time : 3864 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 15:38:21 ; Search time 560 Seconds  
(without alignments)  
8372.206 Million cell updates/sec

Title: US-09-890-782-3

Perfect score: 1 ttcttaaaaaagaagaaat.....ttatatccaaaaaatttcac 792

Sequence: 1

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database :

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1: geneseqn19808:\*  
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3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
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7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	155.2	19.6	924	12	ADP99769
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9	134	16.9	913	10	ADP37188
10	134	16.9	913	12	AD141542
11	134	16.9	913	12	AD001614
12	132.6	16.7	885	3	AAA53744
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15	127.6	16.1	694	10	ADK59746
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## ALIGNMENTS

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AC	AAA53745;	
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KM	secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;	
KW	food colouring; flavouring; fragrance; antimicrobial; pathogenic;	
KM	insecticide; gene expression; modulation; ds.	
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OS	Catharanthus roseus.	
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FH	Key	Location/Qualifiers
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PD	10-AUG-2000.	
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XX		
PI	Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;	
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DR	WPI; 2000-499380/44.	
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XX	P-PSDB; AAY97228.	
PT		
XX		
PT	Modulating level of metabolites and stress resistance in recombinant	
XX	cells for synthesis of plant metabolites such as alkaloids including	
PT	terpenoid indole alkaloids, by providing transcription factor to the	
XX	cell.	



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DT      17-OCT-2000 (first entry)
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KW      Hybridisation assay; genetic mapping; gene expression control;
KW      protein identification; signal transduction pathway; metabolic pathway;
KW      promoter; termination sequence; ss.
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PN      EP1033405-A2.
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PD      06-SEP-2000.
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PF      25-FEB-2000; 2000EP-00301439.
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PR 31-AUG-1999; 99US-0151438P.  
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PR 07-SEP-1999; 99US-0152630P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
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PR 28-SEP-1999; 99US-0156458P.  
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PR 04-OCT-1999; 99US-0157117P.  
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PR 18-OCT-1999; 99US-0159584P.  
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PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
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PR 26-OCT-1999; 99US-0161360P.  
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PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.

PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.  
  
Query Match 17.1%; Score 135.6; DB 3; Length 914;  
Best Local Similarity 64.2%; Pred. No. 2e-26;  
Matches 204; Conservative 0; Mismatches 114; Indels 0; Gaps 0;  
  
QY 233 CGGAAAGCTGTGAGAGATTCTGTGTGGAAACCCCGCAGAACGCGCGGAGAGG 292  
DB 290 CCGTTACCTCTCCGCGGAGAAAGATTAACCTCCGCGCAGAAAGCGAGATGCTCACAG 349  
QY 293 GTTGTTCGAAGATTGGAACCGGTATTAAGCGGCTTAAGCGCGCCCTGTGGGAACTTG 352  
DB 350 CGCCGAGGAGAAAGGAGTGCAGTACAGAGAGTGGAGGAGCGCTGTGGGAAATTG 409  
QY 353 CGGCGAGATTAAGGATCCGAAAGAAAGATCCAGATTGGTTGGTATCATATGAG 412  
DB 410 CGGCGAGATTAAGGATCCGAAAGAAAGATCCAGATTGGTTGGTATCATATGAG 469  
QY 413 CACCTGAGATGAGCATTGGCTTATGATGACCGCGCTTTAATATGCGTGAAG 472  
DB 470 CGCGGAGAGACGCGCGGTGGGTATGACCGAGCGCGCTTTCAGCTCAGAGATGGAAG 529  
QY 473 CTAGGCTTAATTTTCTCATTTGATTGTTTCAATATTTCCGAGCCGCTTAAGTAAC 532  
DB 530 CTAGGCTGAATTTTCCGCAATTGATTGTTTGTATGATGAGCCGCTTAAGTAAGC 589  
QY 533 CGAGAAAGCTTCCCTG 550  
DB 590 CTCGCGTCTGCTCCG 607  
  
RESULT 4  
ID ABZ14410 standard; DNA; 681 BP.  
XX ABZ14410;  
AC ABZ14410;  
XX 21-JAN-2003 (first entry)  
DT  
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2215.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2215.  
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
KW Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX W0200216655-A2.  
FN  
XX 28-FEB-2002.  
PD  
XX 24-AUG-2001; 2001MO-US026685.  
PF  
XX 24-AUG-2000; 2000US-0227866P.  
PR 26-JAN-2001; 2001US-026467P.  
PR 22-JUN-2001; 2001US-0300111P.  
XX  
PA (SGRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Harper JF, Kreps J, Wang X, Zhu T;  
PI WPI; 2002-304127/34.  
DR  
XX  
XX Identifying a stress condition to which a plant cell has been exposed and  
PT producing plants with increased tolerance to these abiotic stresses.  
FT  
XX  
XX Claim 144; SEQ ID NO 2215; 577bp + Sequence Listing; English.  
PS  
CC The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising: (a) contacting nucleic acid  
CC representative of expressed polynucleotides in the plant cell with an  
CC array or probes representative of the plant cell genome; and (b)  
CC detecting a profile of expressed polynucleotides in the plant cell



CC characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
CC with increased tolerance to abiotic stress. The present sequence is that  
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used  
CC in methods of the invention. Note: The sequence data for this patent is  
CC not represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office

SQ Sequence 681 BP; 162 A; 154 C; 205 G; 160 T; 0 U; 0 Other;

Query Match 16.9%; Score 134; DB 6; Length 681;  
Best Local Similarity 63.8%; Pred. No. 4.8e-26;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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Db 191 CCGTACCTCTCCGCGGAGAGAAATTAAGCTCCGCGAGCGAAAGCGAGTGGCTCAACG 250
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QY 293 GTTGTTCGAAGATTGGAAACCGGTAATAGGCGCTTAACGCGCGCGTGGGGGAATTGC 352
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 251 CGCGGAGCGAAGAGGAGATGCAATACAGAGAGATGAGAGAGAGCCCTGGGGAAATTCG 310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 353 CGCGGAGATTAAGCGGATCCGAAAAAGAAAGATCCAGATTTGGTTGGTACATACGAGA 412
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 311 CGCGGAGATTAGGAGATCCGAAAGAAAGAGAGCTAGAGTTGGCTCGGACTTACGAGA 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 413 CACCTGAGATGAGAGATTTGGCTTATGATGACCGCGCTTAATATCGGTGAGCTAAAG 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 371 CGCGGAGAGCGCGCGGTGCGTACGACGAGCGGCGTTTCAGCTCAGAGATCGAAAG 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 473 CTAGGCTTAATTTCTCATTTGATTGTTGCAATATTTCGAGACCGCGTTAGAGTAAC 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 431 CTAGCTGAATTTTCCGCATTTGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 533 CGAGAAAAAGCTTTCCTG 550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 491 CTCGCCGTGCTCGCCGG 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 5

ID ADN73806 standard; cDNA; 681 BP.

AC ADN73806;

DT 15-JUL-2004 (first entry)

DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1701.

KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;

KW growth regulator; animal feed product; thale cress;

OS Arabidopsis thaliana.

PN MO2004035798-A2.

PD 29-APR-2004.

PF 20-OCT-2003; 2003MO-EP011658.

PR 18-OCT-2002; 2002EP-00079408.

PA (CROP-) CROPDESIGN NV.

PI Inze D, De Veylder L, Vlieghe K;

DR MPI: 2004-34846/32.

DR P-PSDB; ADN73807.

PT Altering plant characteristics, useful for producing plants for enzyme or  
PT pharmaceutical production comprises modifying in a plant, expression of  
PT one or more nucleic acids and/or modifying level or activity of one or

PT more proteins.

PS Claim 1; SEQ ID NO 1701; 134pp; English.

CC This invention relates to a novel method for altering one or more plant  
CC characteristic. Specifically, it refers to identifying genes that are up  
CC - or down-regulated in transgenic plants overexpressing the heterodimeric  
CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to  
CC alter plant characteristics accordingly. The present invention describes  
CC generating transgenic plants for the production of growth regulators,  
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where  
CC the altered plant characteristics are selected from increased yield or  
CC biomass, enhanced survival capacity, stress tolerance, plant architecture  
CC or physiology, altered endoreplication, biochemistry, signal  
CC transduction, storage lipid mobilization and/or altered photosynthesis,  
CC each relative to the corresponding wild type plants. Accordingly, these  
CC sequences can also be useful as positive or negative selectable markers  
CC during transformation of cells or tissues. The identified genes play a  
CC role in a variety of biological processes such as DNA replication, cell  
CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as  
CC transcription factors. This polynucleotide sequence is thale cress cDNA  
CC repressed 1.3 fold or more in plants overexpressing the E2Fa/Dpa  
CC transcription factor, given in an exemplification of the invention.

SQ Sequence 681 BP; 162 A; 154 C; 205 G; 160 T; 0 U; 0 Other;

Query Match 16.9%; Score 134; DB 12; Length 681;  
Best Local Similarity 63.8%; Pred. No. 4.8e-26;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 191 CCGTACCTCTCCGCGGAGAGAAATTAAGCTCCGCGAGCGAAAGCGAGTGGCTCAACG 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 293 GTTGTTCGAAGATTGGAAACCGGTAATAGGCGCTTAACGCGCGCGTGGGGGAATTGC 352
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 251 CGCGGAGCGAAGAGGAGATGCAATACAGAGAGATGAGAGAGAGCCCTGGGGAAATTCG 310
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QY 353 CGCGGAGATTAAGCGGATCCGAAAAAGAAAGATCCAGATTTGGTTGGTACATACGAGA 412
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Db 311 CGCGGAGATTAGGAGATCCGAAAGAAAGAGAGCTAGAGTTGGCTCGGACTTACGAGA 370
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QY 413 CACCTGAGATGAGAGATTTGGCTTATGATGACCGCGCTTAATATCGGTGAGCTAAAG 472
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Db 371 CGCGGAGAGCGCGCGGTGCGTACGACGAGCGCGGTTTCAGCTCAGAGATCGAAAG 430
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QY 473 CTAGGCTTAATTTCTCATTTGATTGTTGCAATATTTCGAGACCGCGTTAGAGTAAC 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 431 CTAGCTGAATTTTCCGCATTTGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 533 CGAGAAAAAGCTTTCCTG 550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 491 CTCGCCGTGCTCGCCGG 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 6

ID AB065748 standard; DNA; 685 BP.

AC AB065748;

DT 21-AUG-2002 (first entry)

DE Arabidopsis thaliana polynucleotide SEQ ID NO 325.

KW Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;

KW stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;

OS Arabidopsis thaliana.

PN US2002059663-A1.

PD 16-MAY-2002.  
XX  
XX 26-JAN-2001; 2001US-00770149.  
XX  
XX 27-JAN-2000; 2000US-0178506P.  
XX  
XX (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (TUY/) YU Y.  
PA (RAME/) RAMEKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRICK/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
XX  
XX Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;  
PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;  
PI Hurban P;  
XX  
XX WPI; 2002-479224/51.  
XX  
XX New nucleic acid that hybridizes to Arabidopsis thaliana sequences,  
PT useful e.g. for preparing transgenic plants with increased resistance or  
XX altered metabolism.  
XX  
XX Claim 1; SEQ ID NO 325; 40bp + Sequence Listing; English.  
XX  
XX The invention relates to nucleic acids (I) that hybridise under stringent  
CC conditions to any of 999 sequences (AB065424-AB066422) or their  
CC fragments. (I) are used to express the corresponding polypeptides (II) or  
CC to produce genetically modified plant cells or transgenic plants, which  
CC may have improved resistance to disease or stress, or altered  
CC metabolic/biosynthetic pathways (for production of commercial,  
CC nutritional or medicinal products), or generally any trait of interest,  
CC or can be used to screen for biologically active agents (e.g. fungicides,  
CC insecticides and antibiotics). Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from the USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=99909770149  
XX  
XX Sequence 685 BP; 171 A; 139 C; 202 G; 173 T; 0 U; 0 Other;  
SQ  
Query Match 16.9%; Score 134; DB 6; Length 685;  
Best Local Similarity 63.8%; Pred. No. 4.8e-26;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
QY 233 CGGAAAGCTGTCAAGAGATTCTGTTGCGAAACCCCGCAGAAAGCCGCGGAGAG 292  
DB 73 CCGTACCTCTCCGCGCGGAGAAATTAAGCTCCGCGGAGCGAAGCGTCAACAG 132  
QY 293 GTTGTTCGAAGATTGGAACCGGATTAAGGCGCTTGAACGCGCGCTGGGGGAAGTTCG 352  
DB 133 CGCGGAGGCAAGAGGGATCGACGACAGAGAGAGAGAGCGCTGGGGAATTCG 192  
QY 353 CGCGGAGATTAAGGATCCGAAAAAGAAAGATCCAGAGATTGTTGGTTACATACGAGA 412  
DB 193 CGCGGAGATTAGGATCCGAAAGAGACGAGTGAAGGTTTGGCTCGGACCTTACAGA 252  
QY 413 CACCTGAGATGACGATTCGCTTATGATGACAGCCGCTTAAATATGCGTGAAGCTTAAG 472  
DB 253 CGCGGAGGAGCGCGCGGTGCGTACGACCGAGCGGCGTTTCAAGTCAAGATCCGAAAG 312

QY 473 CTAGGCTTAATTTCTCATTTGATTGTTCCGAAATATTCGAGACCCGTTAGAGTAAAC 532  
DB 313 CTAGCTGAATTTTCCGATTTGATTGTTCTGTAAGATAGCCGCTTAGATTAAGGC 372  
QY 533 CGAGAAAGCTTTCCTG 550  
DB 373 CTCGCCGTGCTCGCCG 390  
RESULT 7  
ID AAC44305 standard; DNA; 781 BP.  
XX  
XX AAC44305;  
AC  
XX 18-OCT-2000 (first entry)  
DT  
XX  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 42374.  
DE  
XX  
XX Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway; metabolic pathway;  
KM promoter; termination sequence; ss.  
XX  
XX Arabidopsis thaliana.  
OS  
XX  
XX EP1033405-A2.  
PN  
XX  
XX 06-SEP-2000.  
PD  
XX  
XX 25-FEB-2000; 2000EP-00301439.  
XX  
XX 25-FEB-1999; 99US-0121825P.  
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PR 23-MAR-1999; 99US-0125788P.  
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PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160880P.  
PR 22-OCT-1999; 99US-0160881P.  
PR 22-OCT-1999; 99US-0160899P.  
PR 22-OCT-1999; 99US-0161044P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161933P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 16.9%; Score 134; DB 3; Length 781;  
Best Local Similarity 63.8%; Pred. No. 5e-26;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
QY 233 CGGAAGCTGTGAGGAGATTCTGTGTGGAACCCCGCAGAGCGCGCGAGAGAG 292

Db 291 CCGTTACTCTCCGCGGAGGAAATTAACCTCCGCGACGAGGCGAGTGCTCACACG 350  
Qy 293 GTTGTTCGAAGATTGAACCGGTATTAAGGCGCTTGAAGCGCGCGCTGGGGGAATTTCG 352  
Db 351 CGCCGAGGAGGAGGAGTCACTACAGAGAGTGAAGAGGCGCGTGGGGGAATTTCG 410  
Qy 353 CGCCGAGGATTAAGGATCCGAAAAGAAAGATCCAGATTTGTTGGGTACATTCGAGA 412  
Db 411 CGCCGAGATTAAGGATCCGAAAAGAAAGATTAAGGATTTGCTCGGGAATTACGAGA 470  
Qy 413 CACCTGAGATGAGATTTGCTTATGATGACCGCGCTTATATGCGTGAAGTAAAG 472  
Db 471 CGCCGAGGAGCGGCGGTGCGTACGACGAGCGCGTTTCAGCTCAGAGGATGAAAG 530  
Qy 473 CTAGGCTTAATTTCTCTCATTTGATTGTTCCGAAATATTTCCGAGCCGTTAGAGTAAAC 532  
Db 531 CTAAAGTGAATTTTCGCGATTTGATTGTTCTTGTAGATGAGCGGTTAGATTAAGC 590  
Qy 533 CGAGAAAACGTTCCCTG 550  
Db 591 CTCGCGCTGCTGCGCGG 608

RESULT 8  
AAD06444 standard; cDNA; 913 BP.  
ID AAD06444;  
AC AAD06444;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
XX Arabidopsis thaliana transcription factor G22 cDNA.  
DE Transcription factor; environmental stress tolerance; gene therapy;  
KM plant structure; plant development; se.  
XX Arabidopsis thaliana.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 81..761  
FT /tag= a  
FT /product= "Arabidopsis thaliana transcription factor"  
XX  
PN W0200136598-A1.  
XX  
PD 25-MAY-2001.  
XX  
PF 14-NOV-2000; 2000MO-US031458.  
XX  
PR 17-NOV-1999; 99US-0166228P.  
PR 17-APR-2000; 2000US-0197899P.  
PR 22-AUG-2000; 2000US-0227439P.  
XX  
XX (MEND-) MENDEL BIOTECHNOLOGY INC.  
PA (PINE/) PINEDA O.  
PA (YUG/) YU G.  
PA (CREE/) CREELMAN R.  
PA (RIEC/) RIECHMAN J L.  
PA (HEAR/) HEARD J.  
PA (RATC/) RATCLIFFE O.  
PA (REUB/) REUBER L.  
PA (KEDD/) KEDDIE J.  
XX  
PI Pineda O, Yu G, Creelman R, Riechmann JL, Heard J, Ratcliffe O;  
PI Reuber L, Keddie J;  
XX  
XX WPI; 2001-336000/35.  
DR P-PSDB; AAE02464.  
XX  
XX Nucleic acids encoding plant transcription factor polypeptides, useful  
PT for altering the environmental stress tolerance characteristics of  
PT plants.  
XX

PS Claim 4; Page 54-55; 116pp; English.  
XX  
XX The present sequence is a cDNA encoding Arabidopsis thaliana  
CC transcription factor. This novel transcription factor is useful for  
CC modifying a plant's phenotype in desirable ways, such as modifying a  
CC plants environmental stress. The transcription factor is encoded by  
CC environmental stress tolerance gene derived from Arabidopsis thaliana.  
CC The transcription factors and the genes encoding them are used to alter  
CC the structure and developmental characteristics of plants such as  
CC soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower,  
CC alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry,  
CC raspberry, cantaloupe, carrot, cauliflower, coffee, onion, cucumber,  
CC eggplant, grapes, honey dew, lettuce, mango, melon, papaya, peas,  
CC peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato.  
CC watermelon, roseaceous fruits and/or vegetable brassicas. These sequences  
CC are also used for modifying traits associated with environmental stress  
CC tolerance, such as freezing, chilling, heat, drought, water saturation,  
CC salt, photoconditons, radiation and ozone. The transcription factors are  
CC used in gene therapy  
XX  
XX Sequence 913 BP; 249 A; 190 C; 236 G; 238 T; 0 U; 0 Other;

Query Match 16.9%; Score 134; DB 4; Length 913;  
Best Local Similarity 63.8%; Pred. No. 5.4e-26;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 233 CGGAAAGCTGTCAAGAGATTCTGTGTGGAAACCCGCGCAGAGCGCGCGAGAG 292  
Db 271 CGGTACTCTCCGCGGAGGAAATTAAGCTCCGCGAGAGGAGATGCTCACACG 330  
Qy 293 GTTGTTCGAAGATTGAACCGGTATTAAGGCGCTTGAAGCGCGCGTGGGGGAATTTCG 352  
Db 331 CGCCGAGGCGAGAGGAGATGAGTACAGAGAGTGAAGGAGGCGCGTGGGGGAATTTCG 390  
Qy 353 CGCGGAGATTAAGGATCCGAAAAGAAAGATCCAGATTTGTTGGTATCATTCGAGA 412  
Db 391 CGCGGAGATTAAGGATCCGAAAAGAAAGATCCAGATTTGTTGGTATCATTCGAGA 450  
Qy 413 CACCTGAGATGAGATTTGCTTATGATGACCGCGCTTATATGCGTGAAGTAAAG 472  
Db 451 CGCCGAGGAGCGGCGGTGCGTACGACGAGCGCGCTTACAGTCAAGAGATGAAAG 510  
Qy 473 CTAGGCTTAATTTCTCTCATTTGATTGTTCCGAAATATTTCCGAGCCGTTAGAGTAAAC 532  
Db 511 CTAAAGTGAATTTTCGCGATTTGATTGTTCTTGTAGATGAGCGGTTAGATTAAGC 570  
Qy 533 CGAGAAAACGTTCCCTG 550  
Db 571 CTCGCGCTGCTGCGCGG 588

RESULT 9  
ADE37188 standard; cDNA; 913 BP.  
ID ADE37188  
XX  
XX ADE37188;  
AC  
XX  
DT 29-JAN-2004 (first entry)  
XX  
XX Plant yield related polynucleotide clone G22.  
DE  
XX  
XX dsf gene; transcription factor; tolerance; environmental condition;  
KM microbial disease; fungal disease; viral disease; pest infestation;  
KM herbicide sensitivity; heavy metal tolerance; heavy metal uptake;  
KM growth improvement; photocondition; nutrient uptake; hormone sensitivity;  
KM transgenic plant.  
XX Arabidopsis thaliana.  
OS  
XX  
XX Key Location/Qualifiers  
FT CDS 81..761  
FT /tag= a  
FT /product= "transcription factor"  
FT

XX MO2003014327-A2.  
 XX  
 XX PD 20-FEB-2003.  
 XX  
 XX PF 09-AUG-2002; 2002WO-US026966.  
 XX  
 XX PR 09-AUG-2001; 2001US-0310847P.  
 XX PR 19-NOV-2001; 2001US-0336049P.  
 XX PR 11-DEC-2001; 2001US-0338692P.  
 XX PR 14-JUN-2002; 2002US-00171468.  
 XX  
 XX (MEND-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 XX PI Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LJ, Dubell AN;  
 XX PI Ratcliffe O, Pineda O, Yu G, Broun PE;  
 XX DR WPI; 2003-256576/25.  
 XX DR P-PSDB; AD837189.  
 XX  
 XX PT New stress-related transcription factor polynucleotides and polypeptides,  
 XX PT useful for producing transgenic plants with e.g. improved tolerance to  
 XX PT diseases or pests, decreased herbicide sensitivity, or improved nutrient  
 XX PT uptake.  
 XX  
 XX PS Disclosure; SEQ ID NO 127; 470pp; English.  
 XX  
 XX CC The invention relates to a number of cDNA sequence and their encoded  
 XX CC proteins which are especially transcription factor cDNAs and their  
 XX CC proteins. The isolated or recombinant polynucleotide is useful for  
 XX CC producing a modified plant with a modified trait, e.g. enhanced tolerance  
 XX CC to environmental conditions, improved tolerance to microbial, fungal or  
 XX CC viral diseases, improved tolerance to pest infestation, decreased  
 XX CC herbicide sensitivity, improved tolerance of heavy metals, or enhanced  
 XX CC ability to take up heavy metals, improved growth under poor  
 XX CC photoconditions, improved nutrient uptake, or reduced hormone  
 XX CC sensitivity. The transgenic plants are useful for growing a progeny plant  
 XX CC comprising the desired trait. The polynucleotides and polypeptides are  
 XX CC also useful in bioinformatic search methods. This sequence represents one  
 XX CC of the cDNAs of the invention.  
 XX  
 XX SQ Sequence 913 BP; 249 A; 190 C; 236 G; 238 T; 0 U; 0 Other;  
 XX  
 XX Query Match 16.9%; Score 134; DB 10; Length 913;  
 XX Best Local Similarity 63.8%; Pred. No. 5,4e-26;  
 XX Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
 XX  
 XX QY 233 CGGAAGCTGTGAGAGATTCTGTGTGGAAACCCCGCAGAAAGCGCGCGAGAG 292  
 XX DB 271 CGGTACCTCTCCGGCGGAGAAATAAGCCTCCGGCGAGAGAGCGATGCTCACACG 330  
 XX QY 293 GTTGTTCGAGATTGGAAACCGGTATAGAGCGCTTACCGCGCGCTGGGGGAAATTGG 352  
 XX DB 331 CGCGAGGAGAAAGGGGATGACAGAGAGAGAGAGAGAGAGCGCTGGGGGAAATTGG 390  
 XX QY 353 CGCGCGAGATTAAGGATCCGAAAGAAAGAGATTCAGGATTTGGTTGGTACATACAGA 412  
 XX DB 391 CGCGCGAGATTAGGATCCGAAAGAAAGAGATTCAGGATTTGGCTCGGAGACTTACAGA 450  
 XX QY 413 CACCTGAGATGAGAGATTCGATATGATGAGCGCGCTTAAATATGCGTGGAGCTAAAG 472  
 XX DB 451 CGCGGAGAGACGGCGCGCTGAGTACAGACGAGCGGCTTACCTAGAGAGATCGAAAG 510  
 XX QY 473 CTAGGCTTAATTTCTCATATTGATTGTTGGAATATTTCCGAGCCCGTTAGAGTAAC 532  
 XX DB 511 CTAGGCTGAATTTTCCCATTTGATTGTTCTTGTAGATTAAGCCGTTAGAGTTAGGC 570  
 XX QY 533 CGAGAAAAGCTTTCCTG 550  
 XX DB 571 CTGCGGTGCTGCGCGG 588

AD141542  
 ID AD141542 standard; DNA; 913 BP.  
 XX  
 XX AC AD141542;  
 XX  
 XX DT 22-APR-2004 (first entry)  
 XX  
 XX DE Plant transcription factor polynucleotide #3.  
 XX  
 XX KW transgenic; plant; enhanced tolerance to abiotic stress;  
 XX KW glyophosphate tolerance; hormone sensitivity; disease resistance;  
 XX KW sugar sensing; flowering; flower structure; stem bifurcation;  
 XX KW branching pattern; apical dominance; trichome; stem morphology;  
 XX KW root growth; root hair; seed development; cell proliferation;  
 XX KW cell differentiation; premature senescence; necrosis; plant size;  
 XX KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;  
 XX KW plant anthocyanin; light response; shade avoidance; bioinformatic;  
 XX KW transcription factor; gene; ds.  
 XX  
 XX OS Arabidopsis thaliana.  
 XX  
 XX XX US2004019927-A1.  
 XX  
 XX PD 29-JAN-2004.  
 XX  
 XX PF 25-FEB-2003; 2003US-00374780.  
 XX  
 XX PR 18-APR-2001; 2001US-00837944.  
 XX  
 XX PA (SHER/) SHERMAN B K.  
 XX PA (RIEC/) RIECHMANN J L.  
 XX PA (JIANG/) JIANG C.  
 XX PA (HEAR/) HEARD J E.  
 XX PA (HAAR/) HAARE V.  
 XX PA (CREE/) CREELMAN R A.  
 XX PA (RATC/) RATCLIFFE O.  
 XX PA (ADAM/) ADAM L J.  
 XX PA (REUB/) REUBER T L.  
 XX PA (KEDD/) KEDDIE J.  
 XX PA (BROU/) BROUN P E.  
 XX PA (PILG/) PILGRIM M L.  
 XX PA (DUBE/) DUBELL A N.  
 XX PA (PINE/) PINEDA O.  
 XX PA (YUGG/) YU G.  
 XX  
 XX PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V,  
 XX PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;  
 XX PI Pilgrim ML, Dubell AN, Pineda O, Yu G;  
 XX DR WPI; 2004-132245/13.  
 XX DR P-PSDB; AD141543.  
 XX  
 XX PT New transgenic plant comprising a recombinant polynucleotide of any one  
 XX PT of more than 500 nucleotide sequences, useful in bioinformatic search  
 XX PT methods.  
 XX  
 XX PS Claim 1; SEQ ID NO 5; 435pp; English.  
 XX  
 XX CC The invention describes a transgenic plant comprising a recombinant  
 XX CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 XX CC defined in the specification or its complement. The method of the  
 XX CC invention can be used to produce a plant having altered traits such as:  
 XX CC enhanced tolerance to abiotic stress; glyophosphate tolerance; hormone  
 XX CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
 XX CC altered flower structure, change in stem bifurcations, altered branching  
 XX CC pattern, reduced apical dominance, reduced trichome density; lack of  
 XX CC trichomes; reduced ectopic trichome development; altered trichome  
 XX CC development; increase in trichome number; altered stem morphology;  
 XX CC increased root growth; increased root hairs; altered seed development;  
 XX CC altered cell proliferation or cell differentiation; rapid development;  
 XX CC premature senescence; increased necrosis; increase in seedling or plant  
 XX CC size; decreased plant size; leaf morphology; seed morphology; seed  
 XX CC biochemistry; increase in root anthocyanins; increase in plant

CC anthocyanins, or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This sequence encodes a plant transcription  
 CC factor that can be used in the creation of a transgenic plant with  
 CC altered traits.

XX Sequence 913 BP; 249 A; 190 C; 236 G; 238 T; 0 U; 0 Other;

Query Match 16.9%; Score 134; DB 12; Length 913;  
 Best Local Similarity 63.8%; Pred. No. 5.4e-26;  
 Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 233 CCGAAAGCTGTCAGAGATTCGTTGTGGAACCCCGCCAGAGCGCGCGAGGAG 292  
 DB 271 CCGTACCTCTCCGGGAGGAAATTAACCTCCGCGAGAGGAGAGTGCTCACACG 330  
 QY 293 GTTGTTCGAAGATTGGAACCGGTATTAAGCGCGTTAGACCGCGCGCGGGAAGTTG 352  
 DB 331 CGCCGAGGAGAAAGGAGATGACATACAGAGAGTGAGGAGGCGCGTGGGGAATTCG 390  
 QY 353 CGCCGAGATTAAGGAGATCCGAAAGAGATCCAGATTGTTGGGTACATACGAGA 412  
 DB 391 CGCCGAGATTAAGGATCCGAAAGAGATCCAGATTGTTGGGTACATACGAGA 450  
 QY 413 CACCTGAGATGAGCATGCTTATGATGACCGCGCTTATATATGCGTGAAGCTAAG 472  
 DB 451 CGCCGAGGAGCGCGGCGGTGGCGTACGACGAGCGCGCTTACAGTACAGAGATGAAAG 510  
 QY 473 CTAGGCTTAATTTCTCTCATTTGATTGTTCCGAATTTTCCGAGCCCGTTAAGTAAAC 532  
 DB 511 CTAAAGCTGAATTTCCGCAATTGATTGTTCTTGAAGTATGAGCGCGTTAAGATTAGC 570  
 QY 533 CGAGAAAGCTTCCCTG 550  
 DB 571 CTGCGCGTGGCTGCGCG 588

# RESULT 11

AD001614  
 ID AD001614 standard; cDNA; 913 BP.

XX AD001614;

XX 01-JUL-2004 (first entry)

XX Thalecress transcription factor cDNA #14.

XX Thalecress; transcription factor; ss; gene; plant; transgenic;  
 KW abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;  
 KW phosphate limitation; potassium limitation; nitrogen limitation;  
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;  
 KW flowering; inflorescence architectural change;  
 KW meristem cell differentiation; phylloclax; apical dominance;  
 KW trichome development; seed development; premature senescence;  
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;  
 KW seed morphology; secondary metabolism; light response; shade avoidance.

XX Arabidopsis thaliana.

XX US2004045049-A1.

XX 04-MAR-2004.

XX 10-APR-2003; 2003US-00412699.

XX 13-SEP-1999; 90US-00394519.

XX 21-JAN-2000; 2000US-00489376.

XX 17-FEB-2000; 2000US-00506720.

XX 22-MAR-2000; 2000US-00533591.

XX 22-MAR-2000; 2000US-00533029.

XX 22-MAR-2000; 2000US-00533030.

XX 22-MAR-2000; 2000US-00533392.

XX 22-MAR-2000; 2000US-00533648.

PR 06-APR-2000; 2000WO-US009448.  
 PR 16-NOV-2000; 2000US-00713994.  
 PR 27-MAR-2001; 2001US-00819142.  
 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JAN-2002; 2002US-00958131.  
 PR 14-JUN-2002; 2002US-00171468.  
 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
 PR 09-AUG-2002; 2002US-00225068.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 25-FEB-2003; 2003US-00374780.

XX (ZHAN)/ ZHANG J.  
 PA (FROM)/ FROM M E.  
 PA (HEAR)/ HEARD J E.  
 PA (RICH)/ RICHMANN J L.  
 PA (ADAM)/ ADAM L J.  
 PA (BROU)/ BROU P E.  
 PA (PINE)/ PINEBA O.  
 PA (REUB)/ REUBER T L.  
 PA (KEDD)/ KEDDIE J S.  
 PA (YUGG)/ YU G.  
 PA (JIANG)/ JIANG C.  
 PA (SAMA)/ SAMAHA R S.  
 PA (PIGR)/ PIGRIM M L.  
 PA (CREE)/ CREELMAN R A.  
 PA (DUBB)/ DUBELL A N.  
 PA (BATC)/ BATCLIFFE O.  
 PA (KUMI)/ KUMIMOTO R.  
 PA (SHER)/ SHERMAN B K.

PI Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Brown PE;  
 PI Pineda O, Reuber TL, Keddle JS, Yu G, Jiang C, Samaha RS;  
 PI Pigrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;  
 PI Sherman BK;

XX WPI; 2004-225755/21.  
 DR P-PSDB; AD001615.

XX New transgenic plant, useful in developing phenotypes with altered or  
 PT improved characteristics or traits.

XX Claim 1; SEQ ID NO 27; 213pp; English.

XX The invention relates to a transgenic plant comprising a recombinant  
 CC polynucleotide having a polynucleotide sequence or its complementary  
 CC sequence comprising a sequence encoding a polypeptide, that initiates  
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,  
 CC Rice, Rape or Corn, comprising any of the sequences appearing as AD001588  
 CC -AD003527 or AD003530-AD003559. Also included are using a transgenic  
 CC plant to grow a progeny plant, an expression cassette (comprising a  
 CC constitutive, inducible or tissue-specific promoter and a recombinant  
 CC polynucleotide described above), a host cell comprising the expression  
 CC cassette, producing a modified plant having a modified trait, identifying  
 CC a factor that is modulated by or interacts with a polypeptide encoded by  
 CC the polynucleotide sequence and identifying at least one downstream  
 CC polynucleotide sequence that is subject to a regulatory effect of any of  
 CC the polypeptides encoded by the polynucleotide described above. The  
 CC transgenic plant is useful for producing a plant that has an altered  
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance  
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance  
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to  
 CC salt, tolerance to phosphate limitation, tolerance to potassium  
 CC limitation, decreased sensitivity to nitrogen limitation), altered  
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
 CC response to ethylene, disease resistance, altered susceptibility to  
 CC Brevia, altered susceptibility to Fusarium, altered susceptibility to  
 CC Brevia, altered susceptibility to Pseudomonas syringae, altered  
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed  
 CC germination and seedling vigor, early flowering, late flowering, extended  
 CC period of flowering, an inflorescence architectural change, a change in  
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell  
 CC differentiation, altered phylloclax, altered branching pattern, reduced

CC apical dominance, reduced trichome density, ectopic trichome development,  
 CC altered trichome development, altered stem morphology, increased root  
 CC growth, increased root hairs, altered stem morphology, altered cell  
 CC proliferation/cell differentiation, premature senescence, delayed  
 CC senescence, lethality, increased necrosis, an increase in seedling or  
 CC plant size, decreased plant size, a change in leaf morphology, increased  
 CC altered leaf development, increased leaf size and mass, glossy leaves,  
 CC leaf cell expansion, change in seed morphology, altered seed coloration,  
 CC increased seed size, decreased seed size, altered seed shape, change in  
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid  
 CC content, increased leaf insoluble sugars, decreased leaf insoluble  
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid  
 CC content, an alteration of leaf glucosinolate content, change in seed  
 CC biochemistry, an increase in seed oil content, decrease in seed oil  
 CC content, increase in seed fatty acid content, decrease in seed fatty acid  
 CC content, increase in seed protein content, decrease in seed protein  
 CC content, alteration in seed prenyl lipid content, increase in seed  
 CC sterols, upregulation of genes involved in secondary metabolism, increase  
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in  
 CC light response or shade avoidance. The present sequence encodes a  
 CC thalictress transcription factor of the invention.

SQ Sequence 913 BP; 249 A; 190 C; 236 G; 238 T; 0 U; 0 Other;  
 Query Match 16.9%; Score 134; DB 12; Length 913;  
 Best Local Similarity 63.8%; Pred. No. 5,4e-26;  
 Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
 QY 233 CGGAAAGCTGTGAGAGATTCTGTGTGGAAACCCCGCAGAAAGCGCGCGAGAG 292  
 DB 271 CGGTACTCTCCGCGGAGAGAAATATAGCTCCGCGAGAGAGAGTGCTCACAG 330  
 QY 293 GTTGTTCGAAGATTGGAACCGGTATTAAGGCGGTAGACCGCGCGCGAGAGTTGC 352  
 DB 331 CGCGAGGCGAAGGGGATGCAATACAGAGAGTGAAGAGAGCGCGTGGGGAATTCG 390  
 QY 353 CGCGAGAGATTAAGGATTCGGAAGAAAGAGATCCAGATTTGGTGGTATACAGAGA 412  
 DB 391 CGCGAGAGATTAGGATTCGGAAGAAAGAGATCCAGATTTGGTGGTATACAGAGA 450  
 QY 413 CACCTGAGATGAGAGATTGGCTTATGATGACCGCGGTTTATATGCGTGAAG 472  
 DB 451 CGCGAGAGAGCGCGGCGTGGCGTACAGACCGGCGGTTTCAAGTCAAGAGATCGAAG 510  
 QY 473 CTAGGCTTAATTTCTCATTTGATTTGTTGGAATATTCGGAACCGGTAGATAAC 532  
 DB 511 CTAGGCTGAATTTTCGCAATTGATTGTTCTTGAAGTATGAGCGGTTAAGATTAGGC 570  
 QY 533 CGAGAAACGTTTCCTG 550  
 DB 571 CTGCGCGTGGCTGCGCG 588

RESULT 12  
 AAA53744  
 ID AAA53744 standard; DNA; 885 BP.  
 XX  
 AC AAA53744;  
 XX  
 DT 19-DEC-2000 (first entry)  
 XX  
 DE Plant transcription factor AP2 domain.  
 XX  
 KW AP2; transcription factor; plant metabolism; metabolite; primary;  
 KW secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;  
 KW food colouring; flavouring; fragrance; antimicrobial; pathogenic;  
 KW insecticide; gene expression; modulation; ds.  
 XX  
 OS Catharanthus roseus.  
 XX  
 FH Key  
 CDS Location/Qualifiers  
 FT 9..641  
 FT /\*tag= a

FT /product= "AP2 polypeptide"  
 XX  
 PN W0200046383-A2.  
 XX  
 PD 10-AUG-2000.  
 XX  
 PF 07-FEB-2000; 2000WO-NL000075.  
 XX  
 PR 05-FEB-1999; 99DK-00000158.  
 PR 10-FEB-1999; 99US-0119388P.  
 XX  
 PA (UYLE-) RIJNSUNIV LEIDEN.  
 XX  
 PI Memelink J, Van Der Fits CTR, Menke FLH, Kijne JW;  
 XX WPI, 2000-499380/44.  
 DR P-PSDB; AAY97227.  
 XX  
 PT Modulating level of metabolites and stress resistance in recombinant  
 PT cells for synthesis of plant metabolites such as alkaloids including  
 PT terpenoid indole alkaloids, by providing transcription factor to the  
 PT cell.  
 XX  
 PS Disclosure; Page 95; 101pp; English.

CC Many plant secondary metabolites have value as pharmaceuticals, food  
 CC colourings, flavours and fragrances. Some plant secondary metabolites are  
 CC linked to plant or plant cell defence mechanisms and may confer to the  
 CC plant antimicrobial activity, protection against UV light, herbivores,  
 CC pathogens, insects and nematodes. Plant secondary metabolites such as  
 CC terpenoid indole alkaloids (TIA) represent a class of pharmaceutically  
 CC useful compounds which naturally occur in many plant species. New methods  
 CC are described which modulate the expression of one or more genes involved  
 CC in the biosynthesis of plant metabolites or their precursors in plant  
 CC cells. The method comprises inserting into a plant cell a sequence  
 CC encoding a transcription factor comprising an AP2 DNA-binding domain and  
 CC by modifying the expression of that transcription factor. Transcription  
 CC factors comprising an AP2 DNA-binding domain are useful as central  
 CC regulators of complex metabolite pathways involving numerous target genes  
 CC for such transcription factors. This means that the yield of commercially  
 CC valuable metabolite compounds can be enhanced and the tolerance of plants  
 CC towards exogenous stress factors can be influenced. The tolerance is useful  
 CC for modulating the level of one or more metabolites. By providing a  
 CC transcription factor to the cell the level of the metabolite is enhanced  
 CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to  
 CC a cell to which the transcription factor is not provided  
 XX  
 SQ Sequence 885 BP; 279 A; 151 C; 175 G; 280 T; 0 U; 0 Other;

Query Match 16.7%; Score 132.6; DB 3; Length 885;  
 Best Local Similarity 74.5%; Pred. No. 1.3e-25;  
 Matches 181; Conservative 0; Mismatches 59; Indels 3; Gaps 1;  
 QY 302 AGGATGGAACCGGTATTAAGGCGGTAGACGGCGCGCGGGGGAAGTTCCGCGCGAG 361  
 DB 373 AGGAATGATTTAGTACCGGTGCGGTTAGACGGCGGCCATGGGGAATTCGCTGCCGAA 432  
 QY 362 TAAAGGATCGAAGAAAGAAAGATCCAGATTGTTGGGTATCATACAGAGACCTGAG 421  
 DB 433 TCAGGGATCCCAAGAGAAAGATGAGATATGTTGGGAATTACGAGACGGCGGAG 492  
 QY 422 ATGACGATTTGGCTTATGATGACCGCGGTTTATATATGCTGAGACTTAAAGCTTAA 481  
 DB 493 ATGCGGATTTAGCTTTCATCAAGCGCGCTTCACTCGTGGTTTACAGAGCTTAA 552  
 QY 482 ATTTTCCTATTGATTGTTGGAATATTTCCGACCGGTTAGAGTAACCGAGAAAC 541  
 DB 553 ATTTCCCAATCTATTGTTGTTCTGCTAA-CTCCGGTTAGAGTAAGTCTTACGCC 609  
 QY 542 GTT 544  
 DB 610 GAT 612

RESULT 13  
 ID AA250843  
 AC AA250843; standard; DNA; 708 BP.  
 XX  
 XX  
 DT 31-MAY-2000 (first entry)  
 XX  
 XX Tobacco salicylic acid inducible gene C18-1.  
 DE Tobacco plant; salicylic acid inducible gene; fungal pathogen;  
 KM SA-inducible gene; transgenic plant; pathogen resistance; C18-1 gene; ds.  
 XX Nicotiana tabacum.  
 OS  
 XX MO200008186-A1.  
 PN  
 XX 17-FEB-2000.  
 PD  
 XX 02-AUG-1999; 99MO-EP005581.  
 PF  
 XX 03-AUG-1998; 98US-0095187P.  
 PR  
 XX (MOGE-) MOGEN INT NV.  
 PA  
 XX Stuiver MH, Jepsen I, Horvath DM, Chua N;  
 PI WPI; 2000-205725/18.  
 DR  
 XX Novel salicylic acid inducible genes from tobacco plants, useful for  
 PT making transgenic plants with enhanced pathogenic resistance.  
 PT  
 XX Claim 1; Page 44; 57pp; English.  
 PS  
 XX The patent discloses fifteen new salicylic acid (SA) inducible genes from  
 CC Nicotiana tabacum, which were identified by differential display PCR.  
 CC Nine of these genes were subcloned and sequenced. Based on different  
 CC kinetics of induction response, these genes were classified into four  
 CC categories, class I, II, III and IV response genes. The SA-inducible  
 CC genes are useful for making transgenic plants with enhanced pathogen  
 CC resistance. The plants incorporating these genes show reduced  
 CC susceptibility to fungal pathogens. The present sequence is a  
 CC specifically claimed SA-inducible gene C18-1 from N. tabacum, which  
 CC belongs to class I  
 XX  
 SQ Sequence 708 BP; 205 A; 124 C; 196 G; 183 T; 0 U; 0 Other;  
 Query Match 16.3%; Score 129.4; DB 3; Length 708;  
 Best Local Similarity 64.2%; Pred. No. 8.6e-25;  
 Matches 210; Conservative 0; Mismatches 116; Indels 1; Gaps 1;  
 QY 245 AGGAGGATTCGTGTGTGGGAAACCCGCGAGAGCGGCGCGAGAGGTTGTTGAAAG 304  
 DB 145 AGAGGAAATTTGTGTTTCCACGAGATCAACAGCGCGCGCGCGGTGAGTTACGA 204  
 QY 305 ATTGGAACCGGTATTAAGGCGCTTGACGGCGCGCTTGCGGGAAGTTGCGCGAGTTAA 364  
 DB 205 GGGGAAAGGCAATTACAGAGGTGTGACGACGCGCTTGCGGGAATTGCGCGAGTTTA 264  
 QY 365 GGGATCCGAAAGAAAGATCCA-GGATTTGTTGGGTATCATPCCGAGACCTGAGAGAT 423  
 DB 265 GGGATCCGCGGAGAAATGAGACTTGGGTTTGGCTTGGAACATACGAAACGATGAGAT 324  
 QY 424 GCAAGCATTTGGCTTATGATGACGCGCGCTTATATGCGTGAAGCTAAAGCTTAAT 483  
 DB 325 GCGCATTTGGCTTATGATTAAGCGCTTATATGATGCGTGAAGCTTAAT 384  
 QY 484 TTTCCTCATTTGATTTGTTGATGATATTTCCGAGCCGCTTGAAGTAAACCGAGAAACGT 543  
 DB 385 TTTCACATAGATGATGCTTTTAAATGAACCGGAAACCGGTTGAGTTACGCGGAAAGACGA 444  
 QY 544 TTCCCTCGGAGCCTTACGACGTCG 570

DB 445 GCGTCGCTGAACCGGCTAGTTCGTCG 471  
 RESULT 14  
 ID ADJ10797  
 AC ADJ10797; standard; DNA; 437 BP.  
 XX  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 XX Recombinant tomato DNA to generate disease resistant plants SegID 193.  
 DE  
 KM genetically engineered; plant; Avr-Pro; avirulent Pto;  
 KM bacterial speck disease; tomato; transgenic; biotic; abiotic stress; ds;  
 KM Pfl.  
 XX  
 XX Lycopersicon esculentum.  
 OS  
 XX US2004006787-A1.  
 PN  
 XX 08-JAN-2004.  
 PD  
 XX 14-JAN-2003; 2003US-00341961.  
 PF  
 XX 14-JAN-2002; 2002US-0348792P.  
 PR  
 XX 20-JUN-2002; 2002US-0390249P.  
 PA  
 XX (MART/) MARTIN G B.  
 PA (MYSO/) MYSOB K K.  
 PA (CRAS/) CRASIA O R.  
 PA (FOLK/) FOLKERTS O.  
 PA (SWIR/) SWIRSKY P.  
 PI Martin GB, Mysore KK, Crasta OR, Folkerts O, Swirsky P;  
 DR WPI; 2004-081759/08.  
 DR  
 XX New genetically engineered plant comprising a recombinant polynucleotide  
 PT showing expression associated with Avr-Pro mediated defense response.  
 PT useful in increasing resistance of plant against bacterial speck disease.  
 PS  
 XX Claim 5; SEQ ID NO 193; 176pp; English.  
 XX  
 CC This invention relates to a method of generating novel genetically  
 CC engineered plants. Specifically, it refers to compositions useful for  
 CC transforming plants with a recombinant polynucleotide or plant gene that  
 CC shows a specific pattern of expression associated with the Avr-Pro  
 CC mediated defense response. Avr-Pro is described as the avirulent Pto gene  
 CC found in Pseudomonas syringae pathovar tomato strain T1(A1),  
 CC which mediates bacterial speck disease in tomato plants. The present  
 CC invention describes identifying genes that are up- or down-regulated in  
 CC the defense response and that are involved in the interaction of Avr-Pro  
 CC with Pto and/or Pfl. As such, these novel recombinant polynucleotides  
 CC can be used to generate transgenic plants that are resistant to bacterial  
 CC speck disease and furthermore exhibit increased resistance against biotic  
 CC and abiotic stresses. This polynucleotide sequence is a recombinant  
 CC tomato polynucleotide used to generate genetically engineered, disease  
 CC resistant plants of the invention.  
 XX  
 SQ Sequence 437 BP; 140 A; 79 C; 123 G; 95 T; 0 U; 0 Other;  
 Query Match 16.2%; Score 128.6; DB 12; Length 437;  
 Best Local Similarity 69.0%; Pred. No. 1.2e-24;  
 Matches 176; Conservative 0; Mismatches 79; Indels 0; Gaps 0;  
 QY 316 TATTAAGGCGGTTAGAGCGGCGCGTGGGGAAGTTGCGCGGAGATTAAGGATCCGAA 375  
 DB 10 TATAGAGCGGTTAGAGCGGCGCGTGGGGAAGTTGCGCGGAGATTAAGGATCCGCGG 69  
 QY 376 AAGAAAGATCCAGATTTGTTGGGTACATACGAGACACTGAGGATCCAGCATTTGCT 435



Db 70 AAGACGAGCTTAGGTTGGCTTGGAACCTACGAAAACAGCTGAAGAGCTGCATTGCT 129  
 Qy 436 TATGATGACGCGCGCTTATATGCGTGAGCTAAAGCTAGTAACTTATTTTCTCATTTG 495  
 Db 130 TATGATTAAGCTCTTATGATGAATGAGATCAAAAGACATTGATTTCCGCGACCGG 189  
 Qy 496 ATTGTTGCAATATTTCCGACCCCGTTAGTAAGTAACCCGAGAAACGTTTCCCTGGGAG 555  
 Db 190 ATCGGTTTGAATGAACCGGACCGGTTTCAGTTACCGCGGAAAAGCGAGATGCCCGGAA 249  
 Qy 556 CCTTTCAGACGTCG 570  
 Db 250 CCGGCAAGCTCGTCG 264

RESULT 15  
 ID ADKS9746  
 AC ADKS9746; standard; DNA; 694 BP.  
 XX  
 XX  
 AC ADKS9746;  
 XX  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Plant DNA sequence which confers altered metabolic characteristic #7129.  
 XX  
 KW altered metabolic characteristic; plant; acid metabolism;  
 KW alcohol metabolism; fatty acid metabolism;  
 KW branched fatty acid metabolism; alkaloid metabolism;  
 KW amino acid metabolism; ester metabolism; glyceride metabolism;  
 KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;  
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
 KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.  
 OS Unidentified.  
 XX  
 PN WO2003020936-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 30-AUG-2002; 2002WO-US027884.  
 XX  
 PR 31-AUG-2001; 2001US-0316471P.  
 XX  
 PA (DOMC) DOW CHEM CO.  
 PA (DOMC) DOW AGROSCIENCES LLC.  
 XX  
 PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;  
 PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Muller BA;  
 DR WPI, 2003-313091/30.  
 XX  
 PT Novel genes that confer altered metabolic characteristics in Nicotiana  
 PT benhamiana plants, useful for altering the levels of metabolites e.g.  
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.  
 XX  
 PS Claim 1; SEQ ID NO 7129; 2576bp; English.  
 XX  
 CC The invention comprises DNA sequences which confer an altered metabolic  
 CC characteristic when they are expressed in a plant. The DNA sequences of  
 CC the invention are useful for producing plants with an altered metabolic  
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,  
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other  
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,  
 CC altered glyceride metabolism, altered phenolic metabolism, altered  
 CC carbohydrate metabolism, altered sterol, oxygenated terpene, or  
 CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon  
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the  
 CC invention may be used to provide disease resistance in a plant and gene  
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a  
 CC DNA sequence of the invention.  
 XX  
 SQ Sequence 694 BP; 220 A; 137 C; 184 G; 153 T; 0 U; 0 Other;

Query Match 16.1%; Score 127.6; DB 10; Length 694;  
 Best Local Similarity 57.9%; Pred. No. 2.7e-24;  
 Matches 226; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 228 AATGCGGAAAGCTGTCCAGAGGATTCGTGTGGGAACCCGCCAGAACCGCGCGG 287  
 Db 275 AAATCGAGCCCAAGGAGAGGAATGTGTGTTCCCGCGGAGACAAACCGCGCC 334  
 Qy 288 AGAGGTTGTTCCAGAGATTGGAACCGGTATTAAGGCGCTTAGACGCGCGCGGAGAA 347  
 Db 335 GCGCACTGAGATPCCGAGGGGAAAGCATTAACAGAGGTGTAGACGACGCGCGGAGAA 394  
 Qy 348 GTTCGGCGCGGAGATTAAGGATCCGAAAAGAAAGATCCAGATTGTGTGGTACATA 407  
 Db 395 ATTTGCGGCGGAGATTAGAGATCCGCGAAGAAATGAGCTAGGGTTTGCTTGAACATA 454  
 Qy 408 CGAGACACCTGAGATGACAGCATTTGCTTATGATGAGCGCGCTTAAATATGCGTGAGC 467  
 Db 455 CGAAACAGATGAAGAGCTGCAATTGCTTATGATTAAGCGGCTTATGAAATGCGCGTTC 514  
 Qy 468 TAAAGCTAGGCTTAATTTCTTCATTGATTTGATTTGAAATATTTCCGACCCGTTAGAGT 527  
 Db 515 AAAGCTCATTTAAATTTCCACATGAAATCGGTTAAATGAACCGAACCAGGTTGAGT 574  
 Qy 528 AAACCGAAGAAACGTTTCCCTGCGGAGCCTTCTAGAGCGTGTCTTTCTTCTTC 587  
 Db 575 CACGGGAAAGACGAGCATCGCTGACCGGCTAGTTGTGGAAAATATGTTACACTTA 634  
 Qy 588 TTGCTGAAAATATGAGGAGAAAGAA 617  
 Db 635 ACGGAGAAAGAAAGCTGTTGCGAGCTGAGAA 664

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 Job time : 565 secs

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 16:52:12 ; Search time 185 Seconds  
(without alignments)  
7005.033 Million cell updates/sec

Title: US-09-890-782-3

Perfect score: 792  
Sequence: 1 ttcttaaaagaagaagaat.....ttatcccaaaaagttcac 792

Scoring table: IDENTITY\_NTC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/prodata/1/ina/6A COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	116.2	14.7	933	4	US-09-202-161B-4	Sequence 4, Appl1
2	110.6	14.0	913	4	US-09-533-029-33	Sequence 33, Appl1
3	103.6	13.1	964	4	US-09-533-029-17	Sequence 17, Appl1
4	102.6	13.0	177	4	US-09-202-161B-19	Sequence 19, Appl1
5	86.6	10.9	177	4	US-09-202-161B-20	Sequence 20, Appl1
6	86.6	10.9	761	4	US-09-202-161B-5	Sequence 5, Appl1
7	80.4	10.2	481	4	US-09-640-211A-1401	Sequence 1401, Ap
8	78.6	9.9	1577	4	US-09-533-029-11	Sequence 11, Appl1
9	73.8	9.3	347	4	US-09-640-211A-1502	Sequence 1502, Ap
10	72.8	9.2	362	4	US-09-640-211A-1293	Sequence 1293, Ap
11	72.6	9.2	330	4	US-09-640-211A-1546	Sequence 1546, Ap
12	72.2	9.1	1163	4	US-09-640-211A-570	Sequence 570, App
13	72.2	9.1	447	4	US-09-640-211A-1872	Sequence 1872, Ap
14	72.2	9.1	447	4	US-09-640-211A-436	Sequence 436, App
15	71.8	9.1	1775	4	US-09-533-029-21	Sequence 21, Appl1
16	68	8.6	1055	4	US-09-640-211A-1459	Sequence 1459, App
17	67.8	8.6	675	4	US-09-640-211A-171	Sequence 171, App
18	66.4	8.4	376	4	US-09-640-211A-1582	Sequence 1582, Ap
19	66.4	8.4	522	4	US-09-640-211A-1582	Sequence 5, Appl1
20	66	8.3	987	4	US-10-102-949-10	Sequence 10, Appl1
21	66	8.3	987	4	US-09-964-850-3	Sequence 3, Appl1
22	66	8.3	1265	3	US-10-102-949-6	Sequence 6, Appl1
23	65.4	8.3	350	4	US-09-640-211A-1642	Sequence 1642, Ap
24	64	8.1	1677	4	US-09-640-211A-219	Sequence 219, App
25	63.8	8.1	232	4	US-09-640-211A-1609	Sequence 1609, Ap
26	63	8.0	551	4	US-09-640-211A-1848	Sequence 1848, Ap
27	63	8.0	551	4	US-09-640-211A-1848	Sequence 1848, Ap

c	28	62.4	7.9	331	4	US-09-640-211A-1762	Sequence 1762, Ap
	29	62.2	7.9	1513	4	US-09-301-665A-9	Sequence 9, Appl1
	30	62.2	7.9	1513	4	US-09-301-217-9	Sequence 9, Appl1
	31	60.2	7.6	523	4	US-09-640-211A-1597	Sequence 1597, Ap
	32	60.2	7.6	530	4	US-09-640-211A-1583	Sequence 1583, Ap
	33	59.8	7.6	353	4	US-09-640-211A-1410	Sequence 1410, Ap
	34	59.6	7.5	1405	4	US-09-202-161B-6	Sequence 6, Appl1
	35	59.4	7.5	1132	3	US-08-894-731-3	Sequence 3, Appl1
	36	58.8	7.4	237	4	US-09-640-211A-466	Sequence 466, App
	37	58.6	7.4	950	4	US-09-640-211A-170	Sequence 170, App
	38	57.8	7.3	368	4	US-09-640-211A-1279	Sequence 1279, App
	39	57.8	7.3	916	4	US-09-640-211A-220	Sequence 220, App
	40	57.8	7.3	1437	4	US-09-301-665A-3	Sequence 3, Appl1
	41	57.8	7.3	1437	4	US-09-301-217-3	Sequence 3, Appl1
	42	56.8	7.2	751	4	US-09-533-029-81	Sequence 81, Appl1
	43	56.4	7.1	296	4	US-09-640-211A-1617	Sequence 1617, Ap
	44	56.2	7.1	7218	1	US-08-232-463-14	Sequence 14, Appl1
	45	56	7.1	326	4	US-09-640-211A-1230	Sequence 1230, Ap

#### ALIGNMENTS

RESULT 1  
US-09-202-161B-4  
Sequence 4, Application US/09202161B  
Patent No. 6653533  
GENERAL INFORMATION:  
APPLICANT: Purdue Research Foundation  
TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS  
FILE REFERENCE: 7024-371  
CURRENT APPLICATION NUMBER: US/09/202,161B  
PRIOR FILING DATE: 1999-06-14  
PRIOR APPLICATION NUMBER: PCT/US97/10382  
PRIOR FILING DATE: 1997-06-12  
PRIOR APPLICATION NUMBER: 60/046,494  
PRIOR FILING DATE: 1997-05-14  
PRIOR APPLICATION NUMBER: 60/019,633  
PRIOR FILING DATE: 1996-06-12  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: ASCII  
SEQ ID NO 4  
LENGTH: 933  
TYPE: DNA  
ORGANISM: Lycopersicon esculentum  
US-09-202-161B-4

Query Match 14.7%; Score 116.2; DB 4; Length 933;  
Best Local Similarity 67.8%; Pred. No. 2.8e-24;  
Matches 177; Conservative 0; Mismatches 83; Indels 1; Gaps 1;

QY	278	CGGCGGCGGAGGAGGTTTTCGAGATTGGAACCGGATTAAGGCGTTAGACGGCGC	337
DB	312	CGGACACTCGGCGGTTGAAACCGAAGAAAGACATTATAGAGCGTTAGACACGTC	371
QY	338	CGTGGGGGAAATTTCGGCGGAGATTAAGGATTCGAAAAGAAAGATCCAGATTGGT	397
DB	372	CGGCGGGAATTTGGCGGAGATTAGATCCGCGAAGAACGAGCTAGGGTTGGC	431
QY	398	TGGGTTCATACGAGACACCTGAGGATGCGCATTTGGCTTATGATGAGCGCGTTAAAT	457
DB	432	TTGGAACGTACGAAACGCTGAAGAGCTGCAATTCCTTATGATTAAGCTCTTATGAA	491
QY	458	TGCGTAGAGCTAAAGCTTAGCTTAATTTCTCATATTGATTTGGTTGGAATATTCGGAC	517
DB	492	TGAGAGATCAAAAGACATTTGAATTTCCGACCGGATCGTTGAAT-GAACCGAA	550
QY	518	CCGTTAGAGTAAACCGGAA	538
DB	551	CCGTTGAGATTACGGGAA	571

RESULT 2

```

US-09-533-029-33
: Sequence 33. Application US/09533029
: Patent No. 6664446
:
: GENERAL INFORMATION:
: APPLICANT: Heard, Jacqueline
: APPLICANT: Brown, Pierre
: APPLICANT: Riechmann, Jose-Luis
: APPLICANT: Keddie, James
: APPLICANT: Pineda, Omaira
: APPLICANT: Adam, Luc
: APPLICANT: Samaha, Raymond
: APPLICANT: Zhang, James
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Ratcliffe, Oliver
: APPLICANT: Pilgrim, Marsha
: APPLICANT: Jiang, Cai-Zhong
: APPLICANT: Reuber, Lynne
: TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
: FILE REFERENCE: M01-010
:
: CURRENT APPLICATION NUMBER: US/09/533,029
: CURRENT FILING DATE: 2000-03-22
: EARLIER APPLICATION NUMBER: 60/125,814
: EARLIER FILING DATE: 1999-03-23
: NUMBER OF SEQ ID NOS: 121
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO 33
: LENGTH: 913
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: OTHER INFORMATION: G1006
: US-09-533-029-33

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Query Match	14.0%;	Score 110.6;	DB 4;	Length 913;
Best Local Similarity	62.5%;	Pred. No. 1.3e-22;		
Matches 173; Conservative	0;	Mismatches 104;	Indels 0;	Gaps 0;

Oy	309	GAACCGGTTATPAAGGGCGTTTGAACGGCGGGCCGTGTGGGGAAAGTTCCGGCGGAGATPAAGGA	368
Db	393	GAAACATTACAGAGAGTAGGACAGAGACCCTGTGGGGAAAATTCGCCGCAGATPACTGA	452
Oy	369	TCCGAAAAAAGAAGATCCAGATTTTGTTGGGTACATACGAGACACTTGAGATGCAAC	428
Db	453	TCCGGCGCAAMATGGAGCTATGAGGTTTGGTTAAGGACGTTTGAGACGGCGGAAGATCGGC	512
Oy	429	AATGGCTTATGATGCAGCCGCGTTTAATATGGGTGAGCTAAAGCTAGCTTAATTTCC	488
Db	513	TTTAGCTTACGATATAGCTGCTTTTGAATGCGTGTTCGCCGCTTATTGAATTTCC	572
Oy	489	TCAATTGATGTTTCGATATTTTCCGAGCCCGTTAGATGAACCCGAGAAAACGTTTTCC	548
Db	573	GTTGAGGGTTAATTCGGGTGAACCTGACC CGGTGGCATCAGCTTAAGAGATCTTCTTC	632
Oy	549	TGCGGACCTTTCACGACGTCGTCGCTTCTTCTTCT	585
Db	633	GTCGTGTCGTGTCGTCCTCTTTCAGTCGTCGTCCT	669

RESULT 3  
US-09-533-029-17  
Sequence 17, Application US/095330229  
Patent No. 6664446  
GENERAL INFORMATION:  
APPLICANT: Heard, Jacqueline  
APPLICANT: Beaud, Pierre  
APPLICANT: Reichmann, Josee-Luis  
APPLICANT: Keddie, James  
APPLICANT: Pineda, Omaira  
APPLICANT: Adam, Luc  
APPLICANT: Samaha, Raymond  
APPLICANT: Zhang, James  
APPLICANT: Yu, Guo-Biang  
APPLICANT: Ratcliffe, Oliver

APPLICANT: Pilgrim, Marsha  
 APPLICANT: Jiang, Cai-Zhong  
 APPLICANT: Reuber, Lynne  
 TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES  
 FILE REFERENCE: MBI-010  
 CURRENT APPLICATION NUMBER: US/09/533,029  
 CURRENT FILING DATE: 2000-03-22  
 EARLIER APPLICATION NUMBER: 60/125,814  
 EARLIER FILING DATE: 1999-03-23  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 17  
 LENGTH: 964  
 TYPE: DNA  
 ORGANISM: *Arabidopsis thaliana*  
 FEATURE:  
 OTHER INFORMATION: G28  
 US-09-533-029-17

Query Match	13.1%;	Score 103.6;	DB 4;	Length 964;
Best Local Similarity	63.8%;	Pred. No. 1.6e-20;		
Matches 157;	Conservative 0;	Mismatches 89;	Indels 0;	Gaps 0;

Qy	CGAAGATTGGAACCGGTATTAAGGCGCTTTAGCCGCGCGCGTGGAGGGAAGTTCCGCGCGG	358
Db	CGCGCAGGAGGAAGACATTATAGAGATGAGACAAAGCCCTGGGGGAAATTTGGCGCGG	546
Qy	AGATAAGGATCCGAAAAAGAAAGATCCAGAGATTGGTTGGTACATACGAGACACTTG	418
Db	AGATTGGAATCCGCGGAAGAACGAGCGTTAGGTTGGTTAGAACGTTTGAAGCGCGCGG	606
Qy	AGGATCAGACATTGGGCTTATGATGTGACGCGGCTTTAATATCCGAGAGCTAAAGCTAGGC	478
Db	AGGACCGCGCGTTGGCTTACGACAGAGCTGCTTTCAGAGTCGATGGTTCCCGCGCTTTGT	666
Qy	TTAATTTTCCATTTGATTGATTGCGAATATTTCCGAGCCCGTTAGAGTAAACCCGAGAA	538
Db	TGAATTTTCCGTTGAGAGTTAATATCAGAGAAACCGGACCCGGTTCGAATCAAGTCMAAGA	726
Qy	AACGTT	544
Db	GATCTT	732

## RESULT 4

```

? Sequence:9, Application US/09202161B
? Parent No. 6651533
? GENERAL INFORMATION:
? APPLICANT: Purdue Research Foundation
? TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
? FILE REFERENCE: 7024-371
? CURRENT APPLICATION NUMBER: US/09/302.161B
? PRIOR FILING DATE: 1999-06-14
? PRIOR APPLICATION NUMBER: PCT/US97/10382
? PRIOR FILING DATE: 1997-06-12
? PRIOR APPLICATION NUMBER: 60/046,494
? PRIOR FILING DATE: 1997-05-14
? PRIOR APPLICATION NUMBER: 60/019,633
? PRIOR FILING DATE: 1996-06-12
? NUMBER OF SEQ ID NOS: 30
? SOFTWARE: ASCII
? SEQ ID NO 19
? LENGTH: 177
? TYPE: DNA
? ORGANISM: Lycopersicon esculentum
US-09-202-161B-19

```

Query Match	13.0%;	Score 102.6;	DB 4;	Length 177;
Best Local Similarity	74.6%;	Pred. No. 1,3-20;		
Matches 129;	Conservative 0;	Mismatches 44;	Indels 0;	Gaps 0
Oy	316	TATTAAGGCGTTAGACGCGCCCGGGGGAAGTTCCGCGCGGAGATTAAGGATTCGAAA	375	

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Db      4 TATAGAGCGCTTACAGACGCGCTCCGTGGGGGAAATTTGGCGGAGATTAAGATCCGCGC 63
QY      376 AAGAAAGATCCAGATTTGGTTGGGTACATACGACACCTAGAGATGACGATTGGCT 435
        64 AAGACGGAGCTTGGGTTGGCTTGGAACTGACGAAACAGCTTAAGAAAGCTGCAATTGCT 123
Db      436 TATGATGACGCGCGCTTATATATGCGGTAGAGCTTAAGCTTAAGCTTAATTTTCC 488
        124 TATGATTAAGCTCTTATATGAAATGAGATGACATCAAAAGCATTGAAATTTCCC 176
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## RESULT 5

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US-09-202-161B-20
; Sequence 20, Application US/09202161B
; Patent No. 6653533
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-371
; CURRENT APPLICATION NUMBER: US/09/202,161B
; CURRENT FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: PCT/US97/10382
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/046,494
; PRIOR FILING DATE: 1997-05-14
; PRIOR APPLICATION NUMBER: 60/019,633
; PRIOR FILING DATE: 1996-06-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: ASCII
; SEQ ID NO 20
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-202-161B-20
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Query Match      10.9%; Score 86.6; DB 4; Length 177;
Best Local Similarity 68.8%; Pred. No. 7.5e-16;
Matches 119; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
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```
QY      316 TATAGAGCGCTTACAGACGCGCGCTGGGGGAGATTCGCGGAGATTAAGGATCCGAA 375
        4 TACAGAGAGATACAGCTGCTCCGTGGGGAATATAGCTCGGAAATTCGCAATTCGCT 63
QY      376 AAGAAAGATCCAGATTTGGTTGGGTACATACGACACCTAGAGATGACGATTGGCT 435
        64 AAGACGGAGCTTGGGTTGGCTTGGAACTGACGAAACAGCTTAAGAAAGCTGCAATTGCT 123
Db      436 TATGATGACGCGCGCTTATATATGCGGTAGAGCTTAAGCTTAAGCTTAATTTTCC 488
        124 TATGATTAAGCTCTTATATGAAATGAGATGACATCAAAAGCATTGAAATTTTCC 176
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## RESULT 6

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US-09-202-161B-5
; Sequence 5, Application US/09202161B
; Patent No. 6653533
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-371
; CURRENT APPLICATION NUMBER: US/09/202,161B
; CURRENT FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: PCT/US97/10382
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/046,494
; PRIOR FILING DATE: 1997-05-14
; PRIOR APPLICATION NUMBER: 60/019,633
; PRIOR FILING DATE: 1996-06-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: ASCII
; SEQ ID NO 5
; LENGTH: 761
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; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-202-161B-5
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Query Match      10.9%; Score 86.6; DB 4; Length 761;
Best Local Similarity 68.8%; Pred. No. 1.7e-15;
Matches 119; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
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```
QY      316 TATAGAGCGCTTACAGACGCGCGCTGGGGGAGATTCGCGGAGATTAAGGATCCGAA 375
        176 TACAGAGAGATACAGCTGCTCCGTGGGGAATATAGCTCGGAAATTCGCAATTCGCT 235
Db      376 AAGAAAGATCCAGATTTGGTTGGGTACATACGACACCTAGAGATGACGATTGGCT 435
        236 AAGACGGAGCTTGGGTTGGCTTGGAACTGACGAAACAGCTTAAGAAAGCTGCAATTGCT 295
QY      436 TATGATGACGCGCGCTTATATATGCGGTAGAGCTTAAGCTTAAGCTTAATTTTCC 488
        296 TATGATTAAGCTCTTATATGAAATGAGATGACATCAAAAGCATTGAAATTTTCC 348
```

## RESULT 7

```
US-09-640-211A-1401/C
; Sequence 1401, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1401
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1401
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```
Query Match      10.2%; Score 80.4; DB 4; Length 481;
Best Local Similarity 67.1%; Pred. No. 9.1e-14;
Matches 114; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
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```
QY      321 GGGCGTTAGACGCGCGCGCTGGGGGAAATTCGCGGCGGAGATTAAGGATCCGAAAGAA 380
        480 GGGCGTTCGCGCGCGCGCTGGGGGAAATTCGCGGCGGAGATTAAGGATCCGAAAGAA 421
Db      381 AGGATCAGAGATTTGGTTGGGTACATACGACACCTAGAGATGACGATTGGCTTAATGA 440
        420 GGGGAGCGCGGTGTGCTGGGACGTTTCGACACGCGGAGAGGAGCGGAGGCTTAACGA 361
QY      441 TGCAGCGCGCTTATATATGCGGTAGAGCTTAAGCTTAAGCTTAATTTTCTTC 490
        360 CCGCGCGCGCTTTCAGGCTCCGCGGAGCAAGGCAATCTGAATCTCCCG 311
```

## RESULT 8

```
US-09-533-029-11
; Sequence 11, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Brown, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Kiedde, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
```



Query Match 9.2%; Score 72.6; DB 4; Length 390;  
Best Local Similarity 56.8%; Pred. No. 1.7e-11;  
Matches 154; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

QY 238 AGCTGTCAGAGATTGTTGGGAAACCCCGCAGAGCGCGCGGAGAGGTTGT 297  
DB 48 AGAAGTGAAGTGTCTCTCTTGGAGATGTGAGAGGCTCAACACCGATTGGGGGG 107  
QY 298 TCAGAGATTGGAACCGGTAAAGGGCGGTAGACGGGGCGCGGGGAAAGTTGGGGCG 357  
DB 108 AGAAGAGAAAAATGTTTACAGAGGTATCAGACAGGCTCCATGAGGAAAAATGGGCTGCG 167  
QY 358 GAGATTAAGGATCGAAGAAAGATCCAGATTGTTGGGTATACATAGACACACT 417  
DB 168 GAGATTGAGATCCAGTAAG---GGGGTTAGGGTTGGCTTGAAGCTTCAACAGCGCA 224  
QY 418 GAGATGACAGATTGGCTTATGATGACCGCGCTTAAATATGCTGAGACTAAAGCTAAG 477  
DB 225 GAGAGAGCCCGCAAGGCTATGATGACGCGCTAAAGATCCGAGGTAAAGAAAGCTAAG 284  
QY 478 CTTAATTTCTCATTTGATTGTTGCGAATA 508  
DB 285 CTTAATTTGCTGATTAATCTGTTCTGTTA 315

## RESULT 12

US-09-640-211A-549  
; Sequence 549, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; LENGTH: 1163  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-640-211A-549

Query Match 9.2%; Score 72.6; DB 4; Length 1163;  
Best Local Similarity 56.8%; Pred. No. 3.1e-11;  
Matches 154; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

QY 238 AGCTGTCAGAGATTGTTGGGAAACCCCGCAGAGCGCGCGGAGAGGTTGT 297  
DB 373 AGAAGTGAAGTGTCTCTCTTGGAGATGTGAGAGGCTCAACACCGATTGGGGGG 432  
QY 298 TCAGAGATTGGAACCGGTAAAGGGCGGTAGACGGGGCGCGGGGAAAGTTGGGGCG 357  
DB 433 AGAAGAGAAAAATGTTTACAGAGGTATCAGACAGGCTCCATGAGGAAAAATGGGCTGCG 492  
QY 358 GAGATTAAGGATCGAAGAAAGATCCAGATTGTTGGGTATACATAGACACACT 417  
DB 493 GAGATTGAGATCCAGTAAG---GGGGTTAGGGTTGGCTTGAAGCTTCAACAGCGCA 549  
QY 418 GAGATGACAGATTGGCTTATGATGACCGCGCTTAAATATGCTGAGACTAAAGCTAAG 477  
DB 550 GAGAGAGCCCGCAAGGCTATGATGACGCGCTAAAGATCCGAGGTAAAGAAAGCTAAG 609  
QY 478 CTTAATTTCTCATTTGATTGTTGCGAATA 508  
DB 610 CTTAATTTGCTGATTAATCTGTTCTGTTA 640

## RESULT 13

US-09-640-211A-570  
; Sequence 570, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; LENGTH: 447  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-640-211A-570

Query Match 9.1%; Score 72.2; DB 4; Length 447;  
Best Local Similarity 62.9%; Pred. No. 2.4e-11;  
Matches 129; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 292 GGTGTTGGAAGATTGGAACCGGTAAAGGGGCTTAGACGGGGCGCGGGGGAAGTTC 351  
DB 65 GGTATTGCAAGGCTCGCAAGCTCTACAGAGGTGAGACAGAGGCACTGGGGGAATGG 124  
QY 352 GCGCGGAGATTAAGGATCCGAAAGAAAGATCCAGATTGTTGGGTATACGAG 411  
DB 125 GTAGCAGAGATCAGATTACC---TAGGAATAGAACCAAGCTCTGGCTGGAACCTTTGAC 181  
QY 412 ACACTGAGATCAGACATTGCTTATGATGACCGCGCTTAAATATGCTGAGCTAA 471  
DB 182 ACAGCAGAAAGAACAGGTTTGCATATGACACAGACAGCTCAACACTAGCTGTGAGTAC 241  
QY 472 GCTAGGCTTAATTTCTCATTTGA 496  
DB 242 GCAAGGCTTAATTTCTCGGACTTGA 266

## RESULT 14

US-09-640-211A-1872  
; Sequence 1872, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; LENGTH: 447  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-640-211A-1872

Query Match 9.1%; Score 72.2; DB 4; Length 447;  
Best Local Similarity 62.9%; Pred. No. 2.4e-11;  
Matches 129; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 292 GGTGTTGGAAGATTGGAACCGGTAAAGGGGCTTAGACGGGGCGCGGGGGAAGTTC 351  
DB 65 GGTATTGCAAGGCTCGCAAGCTCTACAGAGGTGAGACAGAGGCACTGGGGGAATGG 124  
QY 352 GCGCGGAGATTAAGGATCCGAAAGAAAGATCCAGATTGTTGGGTATACGAG 411

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Db      125 GTAGCAGAGATTCGATTACC---TAGGAATAGAACCGAGCTCTGGCTTGAACTTTGAC 181
QY      412 ACACCTGAGGATGACGATTTGGCTTATGATGACGCGCGTTAATATGCGTGAAGCTAA 471
Db      182 ACAGCAGAGAGACGACGCTTTGATATGACACAGCAGCCTACCACTAGTGTGAGTAC 241
QY      472 GCTAGGCTTAATTTTCTCATTTGA 496
Db      242 GCAAGGCTTAATTTTCCGACCTTGA 266
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## RESULT 15

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US-09-640-211A-436
; Sequence 436, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436
; LENGTH: 1775
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-436
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Query Match 9.1%; Score 71.8; DB 4; Length 1775;

Best Local Similarity 58.2%; Pred. No. 6.8e-11;

Matches 146; Conservative 0; Mismatches 102; Indels 3; Gaps 1;

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QY      242 GTCAGAGAGATTCGTGTGGGAACCCGCAAGACGCGCGCGAGAGGTTGTCGA 301
Db      513 GTTCGAGCTTCCTTAGCTCGGGGCTTGATGACCGCGGCCCAAGACGCGGTGAGA 572
QY      302 AGGATTGGAACCGGTATTAAGGCGCTTAAAGCGCGCGCTGCGGGAAGTTCCGCGGAGA 361
Db      573 AGAGGAAGATTGTGTACAGAGGATCAGGCAACGTCCATGCGGGAATGGCTGCAGAGA 632
QY      362 TAGGATCCGAAAGAAAGAGATCCAGATTGTGTGGTACATACGAGACCTGAGG 421
Db      633 TCAGGATCCAGA--AAAGGCGTAAAGGTTGGCTGGTACCTTTAATACGCGGAGG 689
QY      422 ATGACGATTTGCTTATGATGACGCGCGTTAATATGCGTGAAGCTAAGCTAGGCTTA 481
Db      690 AAGCTGCTGGGCTTATGATGACGCTGCACGAAGATCAGAGTAAAGAGCGGAAGTAA 749
QY      482 ATTTTCTCAT 492
Db      750 ATTTGTTGAT 760
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 18:16:17 ; Search time 596 Seconds  
(without alignments)  
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Title: US-09-890-782-3

Perfect score: 792  
Sequence: 1 ttctaaagaagaagaat.....ttatcccaaaaagtccac 792

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135.6	17.1	940	US-10-739-930-299	Sequence 299, App
2	134	16.9	681	US-09-938-842A-2215	Sequence 2215, App
3	134	16.9	681	US-09-938-842A-2215	Sequence 2215, App
4	134	16.9	685	US-09-770-149-325	Sequence 325, App
5	134	16.9	913	US-10-225-068-127	Sequence 127, App
6	134	16.9	913	US-10-374-780A-5	Sequence 5, App
7	134	16.9	913	US-10-412-699B-27	Sequence 27, App
8	129.4	16.3	708	US-09-777-207-1	Sequence 1, App
9	129.4	16.3	437	US-10-341-961A-193	Sequence 193, App
10	118.2	14.9	995	US-10-425-114-29849	Sequence 29849, A
11	118.2	14.9	999	US-10-424-599-30914	Sequence 30914, A

C	12	118.2	14.9	1049	17	US-10-374-780A-477	Sequence 477, App
C	13	118.2	14.9	1049	17	US-10-412-699B-978	Sequence 978, App
C	14	116.2	14.7	933	14	US-10-122-822-4	Sequence 4, App
C	15	115.4	14.6	809	18	US-10-739-930-3666	Sequence 3666, App
C	16	113.6	14.3	736	17	US-10-374-780A-498	Sequence 498, App
C	17	113.6	14.3	736	17	US-10-412-699B-999	Sequence 999, App
C	18	113.6	14.3	736	17	US-10-424-599-32647	Sequence 32647, A
C	19	112.2	14.2	515	17	US-10-374-780A-478	Sequence 478, App
C	20	112.2	14.2	515	17	US-10-424-599-99578	Sequence 99578, A
C	21	112.2	14.2	515	17	US-10-412-699B-979	Sequence 979, App
C	22	111.4	14.1	732	9	US-10-424-599-3501	Sequence 3501, App
C	23	110.6	14.0	732	9	US-09-938-842A-154	Sequence 154, App
C	24	110.6	14.0	859	17	US-10-425-114-14753	Sequence 14753, A
C	25	110.6	14.0	859	17	US-10-533-029-33	Sequence 33, App
C	26	110.6	14.0	913	10	US-09-934-455-415	Sequence 415, App
C	27	110.6	14.0	913	10	US-10-374-780A-2073	Sequence 2073, App
C	28	110.6	14.0	913	17	US-10-412-699B-669	Sequence 669, App
C	29	110.6	14.0	913	17	US-10-412-699B-1831	Sequence 1831, App
C	30	110.6	14.0	8398	18	US-10-810-788A-5	Sequence 5, App
C	31	110.6	14.0	8398	18	US-10-424-599-65880	Sequence 65880, A
C	32	109.4	13.8	548	17	US-10-374-780A-493	Sequence 493, App
C	33	106.4	13.4	1181	17	US-10-412-699B-994	Sequence 994, App
C	34	106.4	13.4	1181	17	US-10-412-699B-994	Sequence 994, App
C	35	104.8	13.2	1424	17	US-10-424-599-77457	Sequence 77457, A
C	36	103.6	13.1	964	10	US-09-934-455-1	Sequence 1, App
C	37	103.6	13.1	964	10	US-10-225-068-195	Sequence 195, App
C	38	103.6	13.1	964	17	US-10-374-780A-9	Sequence 9, App
C	39	103.6	13.1	964	17	US-10-412-699B-37	Sequence 37, App
C	40	103.6	13.1	177	14	US-10-122-822-19	Sequence 19, App
C	41	102.6	12.9	169	17	US-10-341-961A-232	Sequence 232, App
C	42	102.4	12.9	741	9	US-09-938-842A-153	Sequence 153, App
C	43	102	12.9	741	11	US-09-938-842A-153	Sequence 153, App
C	44	102	12.9	962	19	US-10-495-918-101	Sequence 101, App
C	45	102	12.9	962	19	US-10-495-918-101	Sequence 101, App

ALIGNMENTS

RESULT 1  
US-10-739-930-299  
; Sequence 299, Application US/10739930  
; Publication No. US20040216190A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739, 930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 299  
; LENGTH: 940  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; OTHER INFORMATION: Clone ID: ARATH-23APR03-CLUSTER1566\_1  
US-10-739-930-299

Query Match	17.1%;	Score 135.6;	DB 18;	Length 940;
Best Local Similarity	64.2%;	Pred. No. 1.8e25;		
Matches 204;	Conservative 0;	Mismatches 114;	Indels 0;	Gaps 0;
QY	233	CGGAAAGCTGTCAGAGATTCTGTGTGGGAAACCCCGCCAGAAAGCGCGCGAGAG	292	
DB	291	CCGTTACTCTCCGCGGAGAAAGATTAAGCCTCCGCGAGAAAGCGAGTCTCAACG	350	
QY	293	GTTGTTGGAAGATTGGAACCGGTATTAAGGCGCTTGAAGCGCGCGCGAGAGTTGC	352	
DB	351	CGCGGAGGAGAAAGGAGTACGATACAGAGGTGAGGAGGCGCGTGGGGAATTCG	410	
QY	353	CGCGGAGGATTAAGGATTCGAAAGAAAGATTCGAGATTGTTGGTGGATACAGAG	412	

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Qy 413 CACCTAGAGATGACGATTTGCTTATGATGACCGCGCTTATATGCTGGAGCTAAG 472
Db 471 CCGCGAGAGACCGCGGGTGGCGTACGACCGCGCTTACGCTCAGAGATGAAAG 530
Qy 473 CTAGGCTAATTTTCTCATTTGATTGTTGTTGCAATATTTCCGAGCCCGTTAGATAAC 532
Db 531 CTAGGCTAATTTTCCGATTTGATTGTTGTTGTAAGTATGACCGGTTAGATTAGGC 590
Qy 533 CGAGAAAACGTTCCCTG 550
Db 591 CTCGCCGTGCTCGCCGG 608
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## RESULT 2

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US-09-938-842A-2215
; Sequence 2215, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2215
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2215
```

Query Match 16.9%; Score 134; DB 9; Length 681;  
Best Local Similarity 63.8%; Pred. No. 4e-25;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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Qy 233 CGAAAAGCTGTCAAGAGATTCTGTTGGAAACCCGCCAAGACCGCGCCGAGAG 292
Db 191 CCGTTACTCTCCGCGAGAGAAATTAAGCTCCGCGCAGAAAGCGAGTGCCTCACAG 250
Qy 293 GTTGTTCGAAGATTGAAACCGGTATTAAGGCGCTTGAAGCGCGCGCGTGGGGAATTG 352
Db 251 CGCGGAGGCAAGAGGAGATGCACTACAGAGAGTGAAGAGAGCGCGTGGGGAATTG 310
Qy 353 CGCGGAGATTAAAGATCCGAAAAGAAAGATCCAGATTGTTGGTTACATACGAGA 412
Db 311 CGCGGAGATTAGGATCCGAAAGAAAGAGAGCTAGGTTTGGCTCGGACTTACGAGA 370
Qy 413 CACCTAGAGATGACGATTTGCTTATGATGACCGCGCTTAAATATGCTGAGCTAAG 472
Db 371 CGCGGAGAGACGCGGGTGGCGTACGACCGCGCTTACGCTCAGAGATGAAAG 430
Qy 473 CTAGGCTAATTTTCTCATTTGATTGTTGTTGCAATATTTCCGAGCCCGTTAGATAAC 532
Db 431 CTAGGCTAATTTTCCGATTTGATTGTTGTTGTAAGTATGACCGGTTAGATTAGGC 490
Qy 533 CGAGAAAACGTTCCCTG 550
Db 491 CTCGCCGTGCTCGCCGG 508
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RESULT 3  
US-09-938-842A-2215

```
; Sequence 2215, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2215
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2215
```

Query Match 16.9%; Score 134; DB 11; Length 681;  
Best Local Similarity 63.8%; Pred. No. 4e-25;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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Qy 233 CGAAAAGCTGTCAAGAGATTCTGTTGGAAACCCGCCAAGACCGCGCCGAGAG 292
Db 191 CCGTTACTCTCCGCGAGAGAAATTAAGCTCCGCGCAGAAAGCGAGTGCCTCACAG 250
Qy 293 GTTGTTCGAAGATTGAAACCGGTATTAAGGCGCTTGAAGCGCGCGCGTGGGGAATTG 352
Db 251 CGCGGAGGCAAGAGGAGTCACTACAGAGATGAGAGAGCGCGTGGGGAATTG 310
Qy 353 CGCGGAGATTAAAGATCCGAAAAGAAAGATCCAGATTGTTGGTTACATACGAGA 412
Db 311 CGCGGAGATTAGGATCCGAAAGAAAGAGAGCTAGGTTTGGCTCGGACTTACGAGA 370
Qy 413 CACCTAGAGATGACGATTTGCTTATGATGACCGCGCTTAAATATGCTGAGCTAAG 472
Db 371 CGCGGAGAGACGCGGGTGGCGTACGACCGCGCTTACGCTCAGAGATGAAAG 430
Qy 473 CTAGGCTAATTTTCTCATTTGATTGTTGTTGCAATATTTCCGAGCCCGTTAGATAAC 532
Db 431 CTAGGCTAATTTTCCGATTTGATTGTTGTTGTAAGTATGACCGGTTAGATTAGGC 490
Qy 533 CGAGAAAACGTTCCCTG 550
Db 491 CTCGCCGTGCTCGCCGG 508
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## RESULT 4

```
US-09-770-149-325
; Sequence 325, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
```

```

? APPLICANT: Slader, Ted
? APPLICANT: Davis, Keith R.
? APPLICANT: Allen, Keith
? APPLICANT: Hoffman, Neil
? APPLICANT: Huzdan, Patrick
? TITLE OF INVENTION: Expressed Sequences of Arabidopsis
? TITLE OF INVENTION: thaliana
? FILE REFERENCE: 2024 (PARA-013PRV)
? CURRENT APPLICATION NUMBER: US/09/770,149
? CURRENT FILING DATE: 2001-01-26
? PRIOR APPLICATION NUMBER: 60/1178,506
? PRIOR FILING DATE: 2000-01-27
? NUMBER OF SEQ ID NOS: 999
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 325
? LENGTH: 685
? TYPE: DNA
? ORGANISM: Arabidopsis thaliana
US-09-770-149-325

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Query Match	16.9%	Score 134	DB 9	Length 685
Best Local Similarity	63.8%	Pred No. 4.1e-25		
Matches 203; Conservative	0	Mismatches 115	Indels 0	Gaps 0

Qy	233	CGGAAGCTGTGAGGAGATTCTGTGTGGAAACCCGCGAGAAGCGCGCGGAGAG	292
Db	73	CGGTAACTCTCCGGCGAAGAAATAAGCCTCCGGGACGAAGCGAATGGCTCACACG	132
Qy	233	GTTGTTCGAAGATTGGAACCGGTATTAAGGGCTTTAGACGCGCGCGCTGGGGGAAAGTTG	352
Db	133	CGCCGAGCGAAGAGGGAGATGCAGTATACAGAGATGAGAGAGAGCGCTGGGGGAAATTG	192
Qy	353	CGGCGAGATTAAGGGATCCGAAAGAAAGAAAGATCCAGATTTGGTTGGTGATACACGA	412
Db	153	CGGCGGAGATTAGGGATCCGAAGAAAGAGACTAGGTTTGGCTCGGGAATTACAGA	252
Qy	413	CACCTGAGAGATCAGATTTGGCTTATGATGACAGCCGCTTTAATATGCTGGAGCTAAAG	472
Db	253	CGCCGAGAGACGCGCGGTGGCGTACGACCGAGCCGCTTACGCTACAGAGATCGAAAG	312
Qy	473	CTAGGCTTAATTTTCTCATTTGATTTGTTTCGAATATTTCCGAGACCGTATAGATAAC	532
Db	313	CTAAGCTGAATTTTCCGACTTTGATTGATTTGTTCTTTGAATATGAGCCGTTAGAGATTAGG	372
Qy	533	CGAGAAACGTTTCCCTG	550
Db	373	CTGCGCGTGCCTGCGG	390

RESULT 5  
US-10-225-068-127  
Sequence 127, Application US/10/225068  
Publication No. US20030217383A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Heard, Jacqueline E.  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Adam, Luc J.  
APPLICANT: Dubbel, Arnold T.  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Pineda, Omalta  
APPLICANT: Yu, Guo-Piang  
APPLICANT: Brown, Pierre E.  
TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND  
TITLE OF INVENTION: POLYPEPTIDES IN PLANTS  
FILE REFERENCE: 514442002040  
CURRENT APPLICATION NUMBER: US/10/225, 068  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 60/310, 847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 60/336, 049

```

? PRIOR FILING DATE: 2001-11-19
? PRIOR APPLICATION NUMBER: 60/338,692
? PRIOR FILING DATE: 2001-12-11
? PRIOR APPLICATION NUMBER: 10/171,468
? PRIOR FILING DATE: 2002-06-14
? NUMBER OF SEQ ID NOS: 246
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 127
? LENGTH: 913
? TYPE: DNA
? ORGANISM: Arabidopsis thaliana
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (81)...(761)
US-10-225-068-127

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Query Match	16.9%	Score 134	DB 17	Length 913
Best Local Similarity	63.8%	Pred. NO. 4.7e-25		
Matches 203	Conservative	0	Mismatches 115	Indels 0
				Gaps 0

Oy	233	CGAAGACGTGACAGAGATTCTGTGTGGAGACCCCGCAGAGCGCGCGGACGAG	252
Db	271	CGTTTACCTCTCCGGGGAGGAAAATAAGCTCCGGCGACCAAGAGCGAGTGCACACG	330
Oy	293	GTTGTTCGAAGATTGAAACCGGTATAAGGCGGTTAAGCGCGCGCGTGGGGGAAGTTG	352
Db	331	CGCCGAGCGAAGAGGGGATGCATTCAGAGAGTGTAGAGAGAGCGCCGTGGGGGAAATTCG	390
Oy	353	CGCGGAGATTAAGGATCGAAAAAGAAAGATCCAGATTGTGGTTACATACAGA	412
Db	391	CGCGCGAGTTTAGGATTCGAAAGAAAGACGAGCTAGGGTTTGGCTCGGACCTTACAGA	450
Oy	413	CACCTGAGATCAGACATTTGGCTTATGATGACGCCGCGTTTAAATATGCGTGGACGTTAAG	472
Db	451	CGCGGAGAGACCGCGGTGGCGGTACGACCGAGCGGCGTTTCAAGCTCAGAGGATCGAAAG	510
Oy	473	CTTAGGCTTAATTTTCTCATTTGATGTGTGGAATATTTCCGAGCCCGTTAGAGTAAC	532
Db	511	CTTAGCTGAATTTTCCGATTTGATGTGTTCTTGTAGATAGACCGGTTAGAGATTAGGC	570
Oy	533	CGAGAAAAGTTTCCCTG	550
Db	571	CTCGCCGTGCTGCGCG	588

RESULT 6  
US-10-374-780A-5  
Sequence 5, Application US/10374780A  
Publication No. US20040019927A1  
GENERAL INFORMATION:  
APPLICANT: Sherman, Bradley K  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Heard, Jacqueline E  
APPLICANT: Haake, Volker  
APPLICANT: Creelman, Robert A  
APPLICANT: Raccliffe, Oliver  
APPLICANT: Adam, Luc J  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddie, James  
APPLICANT: Brown, Pierre E  
APPLICANT: Pilgrim, Marsha L  
APPLICANT: Dubell III, Arnold T  
APPLICANT: Pineda, Omarita  
APPLICANT: Yu, Guo-Liang  
TITLE OR INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
FILE REFERENCE: MEI-0047 CIP  
CURRENT APPLICATION NUMBER: US/10/374,780A  
CURRENT FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: 09/837,944  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09

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; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G22
US-10-374-780A-5

```

```

Query Match      16.9%; Score 134; DB 17; Length 913;
Best Local Similarity 63.8%; Pred. No. 4,7e-25;
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

```

```

QY 233 CGGAAAGCTGTCAAGAGATTCTGTGTGGGAAACCCCGCCAGAAAGCGCGCCGAGAG 292
DB 271 CGGTACCTCTCCGGGAGGAAATTAAGCTCTCCGCGCAAGAGCGAGTGCCTCACACG 330
QY 293 GTTGTTCGAAGATTGGAACCGGTATTAAGGCGCTTAGACGCGCGCGCTGAGGAAATTG 352
DB 331 CCGCCAGAGAGAGAGGAGTACAGTACAGAGAGTACAGAGAGAGCGCGCTGAGGAAATTG 390
QY 353 CGGCGAGATTAAGGAGATTCGAAAGAAAGAAAGATCCAGAGATTTGTTGGGTACATACGAG 412
DB 391 CGGCGAGATTAAGGAGATTCGAAAGAAAGAAAGATCCAGAGATTTGTTGGGTACATACGAG 450
QY 413 CACCTGAGAGATGACAGATTGGCTTATGATGACCGCGCTTAAATATGCTGAGAGTAAAG 472
DB 451 CGCCGAGAGAGCGGGGGGCGTACGACCGAGCGCGCTTCAAGCTCAGAGAGATCGAAG 510
QY 473 CTAGGCTTAATTTCTCATTTGATTGTTGATATATTTCCGAGCCCGTTAGAGTAAAC 532
DB 511 CTAAAGTGAATTTCCGCAATTTGATTGTTCTTTGTAAGTATGAGCCGTTAGATTAGGC 570
QY 533 CGAGAAACGTTTCCTG 550
DB 571 CTCGCCGTGCTCGCCG 588

```

## RESULT 7

```

US-10-412-699B-27
; Sequence 27, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samana, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.

```

```

; APPLICANT: DuBell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kimimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G22
US-10-412-699B-27

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```

Query Match      16.9%; Score 134; DB 17; Length 913;
Best Local Similarity 63.8%; Pred. No. 4,7e-25;
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

```

```

QY 233 CGGAAAGCTGTCAAGAGATTCTGTGTGGGAAACCCCGCCAGAAAGCGCGCCGAGAG 292
DB 271 CGGTACCTCTCCGGGAGGAAATTAAGCTCTCCGCGCAAGAGCGAGTGCCTCACACG 330
QY 293 GTTGTTCGAAGATTGGAACCGGTATTAAGGCGCTTAGACGCGCGCTGAGGAAATTG 352
DB 331 CCGCCAGAGAGAGAGGAGTACAGTACAGAGAGTACAGAGAGAGCGCGCTGAGGAAATTG 390
QY 353 CGGCGAGATTAAGGAGATTCGAAAGAAAGAAAGATCCAGAGATTTGTTGGGTACATACGAG 412
DB 391 CGGCGAGATTAAGGAGATTCGAAAGAAAGAAAGATCCAGAGATTTGTTGGGTACATACGAG 450
QY 413 CACCTGAGAGATGACAGATTGGCTTATGATGACCGCGCTTAAATATGCTGAGAGTAAAG 472
DB 451 CGCCGAGAGAGCGGGGGGCGTACGACCGAGCGCGCTTCAAGCTCAGAGAGATCGAAG 510
QY 473 CTAGGCTTAATTTCTCATTTGATTGTTGATATATTTCCGAGCCCGTTAGAGTAAAC 532
DB 511 CTAAAGTGAATTTCCGCAATTTGATTGTTCTTTGTAAGTATGAGCCGTTAGATTAGGC 570
QY 533 CGAGAAACGTTTCCTG 550
DB 571 CTCGCCGTGCTCGCCG 588

```

## RESULT 8

```

US-09-777-207-1
; Sequence 1, Application US/09777207
; Publication No. US20020039780A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Horvath, Diana M.
; APPLICANT: Chua, Nam-Hai
; APPLICANT: Stuijver, Maarten H.
; APPLICANT: Jepsen, Ian Salicylic Acid Inducible Genes and Promoters
; FILE REFERENCE: PB/5-50067A
; CURRENT APPLICATION NUMBER: US/09/777,207
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US60/095,187
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-777-207-1

```

```

Query Match      16.3%; Score 129.4; DB 9; Length 708;
Best Local Similarity 64.2%; Pred. No. 6,9e-24;
Matches 210; Conservative 0; Mismatches 116; Indels 1; Gaps 1;

```

```

QY 245 AGGAGATTCTGTGTGGGAGACCCCGCAGAGCGCGCGGAGAGAGTTGTTGAAAG 304
    |||||
DB 145 AGGAGAAATTGTGTTCCTCCAGCGATACACGCGCGCGCGCTGAGTTACCGA 204

QY 305 ATTGGAACGGTATAGAGCGGTAGACGCGCGCGGTGGGAAAGTTGCGCGCGAGTTAA 364
    |||||
DB 205 GGGGAGGAGATTACAGAGGTTAGACGAGCGCTTGGGGGAAATTGGCGCGAGATTAA 264

QY 365 GGGATCCGAAAAAGAAAGATCCA-GGATTGGTGGGTACATACAGACACCTCGAGGAT 423
    |||||
DB 265 GGGATCCGCGGAGAAATGAGCTAGAGCTTTGGCTTGAACATACGAAACAGATGAAGAT 324

QY 424 GGAGATTGGCTTATGATGAGCGCGGTATATATGCTGAGACTAAAGCTTAGCTTAAT 483
    |||||
DB 325 GCTGCAATGCTTATGATTAAGCGGCTTATAGATGCTTCAAAAGCTCAATTTAAAT 384

QY 484 TTTCCTCATTTGATTGGTTCGAAATATTTCCGACCCGTTAGAGTAAACCGAGAAAAGCT 543
    |||||
DB 385 TTTCACATAGAGATCGGTTAAATGAACCGGAAACCGGTTGAGATTACGCGGAAAGACGA 444

QY 544 TTCCCTGCGGAGCGCTTACGAGCTCG 570
    |||||
DB 445 GCCTCCCTGACCGGCTAGTCTGCTG 471

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```

RESULT 9
US-10-341-961A-193

```

```

; Sequence 193, Application US/10341961A
; Publication No. US20040006787A1
; GENERAL INFORMATION:
; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
; APPLICANT: Curagen Corporation
; APPLICANT: Crasera, Oswald
; APPLICANT: Swireky, Peter
; APPLICANT: Mysore, Kiran
; APPLICANT: Folkerts, Otto
; APPLICANT: Martin, Gregory
; APPLICANT: Ekengren, Sophia
; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOC
; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE
; FILE REFERENCE: BTI 67A2
; CURRENT APPLICATION NUMBER: US/10/341,961A
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: 60390249
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60261029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60348792
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.1

```

```

; SEQ ID NO 193
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-341-961A-193

```

```

Query Match      16.2%; Score 128.6; DB 17; Length 437;
Best Local Similarity 69.0%; Pred. No. 8.8e-24;
Matches 176; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

```

```

QY 316 TATAGAGCGCTTAGACGCGCGCGGTGGGAAAGTTGCGCGCGAGATTAAGGATCCGAAA 375
    |||||
DB 10 TATAGAGCGCTTAGACGCGCGCGGTGGGAAATTTGCGCGGAGATTAGAGATCCGGCG 69

QY 376 AAGAAAGATCCAGATTTGGTGGTACATAGAGACACCTAGAGATGACATTTGGCT 435
    |||||
DB 70 AAGAACGAGCTTAGGCTTGGCTTGGAAAGTAAACAGCTGAAAGCTGCAATTTGCT 129

QY 436 TATGATGACGCGCGCTTATATATGCTGAGAGCTTAAGCTTAAGCTTAATTTCTCATTTG 495
    |||||
DB 130 TATGATTAAGCTTCTTATAGATGAGAGATCAAAAGCATTTGATTTCCGCGACCGG 189

QY 496 ATTGATTGAAATTTCCGAGCCCGTTAGAGTAAACCGAGAAACGTTTCCCTGCGAG 555
    |||||
DB 190 ATCGTTTGAATGAACCGAGCCGCTTGAAGTAAAGCGGAAAGCGAGATGCGCGGAA 249

QY 556 CTTTCTACAGCTCG 570
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DB 250 CCGCAAGCTCTGCTG 264

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RESULT 10
US-10-425-114-29849

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; Sequence 29849, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29849
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMROPIC008H09_FLI
US-10-425-114-29849

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Query Match      14.9%; Score 118.2; DB 17; Length 995;
Best Local Similarity 72.5%; Pred. No. 8e-21;
Matches 153; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

```

```

QY 297 TTGGAAGATTGGAACCGGTATTAAGCGCTTGAACGCGCGCGGTGGGAAAGTTGCGCGC 356
    |||||
DB 390 TCCAAAGAGGGGTTGAGCTACCGAGCGTGCAGAGAGCGCGTGGGAAAGTATCGGC 449

QY 357 GGAGATTAAGGATCCGAAAAAGAAAGATCCAGATTTGGTGGTATACGAGACACC 416
    |||||
DB 450 GGAGATTAAGGACACTTAAGAGAGATGTGAGAGTGTGGCTTGAACCTAGAAACCGC 509

QY 417 TGAGATGAGCATTTGGCTTATGATGACACCGCGTTTATATGCGTGAAGCTTAAGCTAG 476
    |||||
DB 510 TGAGATGAGCATTTAGCTTATGATGACACTGATTAAGATGCGGCGCTCAAAAGCTAA 569

QY 477 GCTTAATTTTCTCATTTGATTTGTTGAAT 507

```



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; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 978
; LENGTH: 1049
; TYPE: DNA
; ORGANISM: Glycine max
US-10-412-699B-978
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Query Match 14.9%; Score 118.2; DB 17; Length 1049;
Best Local Similarity 72.5%; Pred. No. 8.2e-21;
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Matches 153; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
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QY 297 TTGAAGATTGTAACCGGATTAAGGCGTTAGACGGCGCGCGTGGGGAAGTTCCGGCG 356
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 649 TCAAGAAAGGGTTGAGCTACGAGCGCTGCGAGAGGCGCTGGGGAAGTATGCGGC 590
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 357 GGAAGTAAGGATCCGAAAAAAGAGATCAGAGATTGGTTGGGTACATACGAGACCC 416
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 589 GGAAGTAAGGATCAGTAAAGAGATGCTGAGAGTGTGCTTGAACCTACGAAACCGC 530
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 417 TAGAGTAGAGCTTGGCTTATATGACGCCGCTTAAATATCGTGAAGTAAAGCTAG 476
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 529 TAGAGTAGAGCTTGGCTTATATGACGCCGCTTAAATATCGTGAAGTAAAGCTAG 470
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 477 GCTTAATTTCTCATTTGATGTTGCTGAAT 507
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 469 GCTGAATTTCTCATTTGATGTTGCTGAAT 439
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RESULT 14
US-10-122-822-4
; Sequence 4, Application US/10122822
; Publication No. US20030084477A1
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-511
; CURRENT APPLICATION NUMBER: US/10/122,822
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/202,161
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: PCT/US97/10382
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/046,494
; PRIOR FILING DATE: 1997-05-14
; PRIOR APPLICATION NUMBER: 60/019,633
; PRIOR FILING DATE: 1996-06-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: ASCII
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; SEQ ID NO 4
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-122-822-4
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Query Match 14.7%; Score 116.2; DB 14; Length 933;
Best Local Similarity 67.8%; Pred. No. 2.6e-20;
Matches 177; Conservative 0; Mismatches 83; Indels 1; Gaps 1;
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QY 278 CGGCGCCCGGAGAGGTTGTTGCAAGATTGAAACCGGTATTAAGGCGCTTAAAGCGCGC 337
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 312 CGGCAAGCTCCGCGCGCTGAAACACGAAAAAAGACATTAATAGAGCGTTAGACAGCGTC 371
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 338 CGTGGGGGAAGTTCCGGCGGAGATTAAGGATCCGAAAAAAGATCCAGATTTGCT 397
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 372 CGTGGGGGAATTTGGCGGAGATTAGATCCGCGAAGACGAGCTTAAGGTTGGC 431
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 398 TGGGTACATACGAGACCTGAGATGACGATTTGCTTATGATGACCGCGTTTATA 457
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 432 TTGAACGTAACGAAAGCTGAAAGAGCTGCAATTCCTTATGATTAAGCTGTTATGAA 491
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 458 TGGGTGAGCTAAAGCTTAAGCTTAATTTCTCATTTGATTTGTTGCAATATTTCCGAC 517
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 492 TGAGAGATCAAAAGACATTTGAATTTCCGACCGGATCGGTTGAAT-GAACCGAA 550
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 518 CGCTTAGAGTAAACCCGAGAA 538
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 551 CGCTTAGAGTAAACCCGAGAA 571
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## RESULT 15

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US-10-739-930-3666
; Sequence 3666, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kowalcik, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 3666
; LENGTH: 809
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: GLVMA-23APR03-CLUSTER5319_2
US-10-739-930-3666
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Query Match 14.6%; Score 115.4; DB 18; Length 809;
Best Local Similarity 74.1%; Pred. No. 4e-20;
Matches 146; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
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QY 307 TGAACCGGTATTAAGCGCTTAAGACGCGCGCGTGGGGAAGTTCCGCGCGGATTAAG 366
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 296 TGAACCGGTATTAAGCGCGCGCTGAAGCGCTTGAACCTTGGGGAAGTTCCGCGCGGAAATAGA 355
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 367 GATCCGAAAAAAGAAAGATCCAGATTTGGTTGGGTACATACGAGACACTGAGATGCA 426
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 356 GATCCGAAAAAAGAAAGATGCTGATGATATGAGCTTTGGACCTTACGAACTGAAAGAAAGCG 415
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 427 GATTTGCTTATGATGACCGCGGTAAATATGCTGAGACTTAAGCTAAGCTTAATTTT 486
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 416 GGTATGCTTATGATGAGCTGCTTTAAGATCGTGGACGAAAGCTAAGTAAATTTT 475
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 487 CCTCATTTGATTGCTTC 503
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 476 CTTCACTCATTTGCTTC 492
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Search completed: March 7, 2005, 20:36:10

Tue Mar 8 08:51:45 2005

us-09-890-782-3.rnpb

Page 8

Job time : 599 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 16:48:09 ; Search time 3384 Seconds  
(without alignments)  
8908.653 Million cell updates/sec

Title: US-09-890-782-3

Perfect score: 792  
Sequence: 1 ttcttaaaagaagaagaat.....ttatcccaaaaagttcac 792

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hnc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g881:\*  
9: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	161	20.3	605	7	CK715561 LERSF01B0
2	154.6	19.5	944	7	CN385373 LERTR03G2
3	153	19.3	673	7	CN385772 LERTR0410
4	152.4	19.2	760	7	CK936905 CGF100451
5	134	16.9	903	3	CNS0A88X
6	133	16.8	563	1	AV552445
7	133	16.8	591	2	BE449392
8	133	16.8	663	1	AV822925
9	132.8	16.8	490	6	CA520877
10	132.6	16.7	636	6	CB078370
11	130.2	16.4	903	2	BE275652
12	129.8	16.4	652	4	BG128566
13	128.6	16.2	437	1	AT771213
14	128.2	16.2	575	2	AM034216
15	128	16.2	633	2	AM584731
16	128	16.2	633	2	AM980654
17	128	16.2	705	4	BG587407
18	128	16.2	707	2	BG647799
19	128	16.2	798	6	CA922634
20	127.6	16.1	930	7	CK288039
21	126.6	16.0	585	7	CF090946
22	126	15.9	842	7	CK276642
23	126	15.9	870	7	CK258279
C 24	125.4	15.8	775	7	CK278893

C 25	125.4	15.8	805	7	CN214825
26	125.4	15.8	857	7	CK278892
27	125.4	15.8	946	7	CK277725
28	125	15.8	703	7	CF088650
C 29	124.4	15.7	655	7	CK258280
C 30	124.4	15.7	739	6	CA920051
C 31	123.8	15.6	809	6	CD574882
C 32	123.4	15.6	622	5	BO517083
C 33	123.4	15.6	652	5	BO517082
34	123.4	15.6	696	7	CF091941
35	123.4	15.6	841	5	BQ047502
C 36	123.4	15.6	949	7	CK268018
C 37	123.4	15.6	980	7	CK268019
C 38	122.8	15.5	687	4	BG584897
39	122.8	15.5	794	6	CF069648
40	122.8	15.5	818	4	BG582281
C 41	122.6	15.5	774	7	CO112337
42	122.6	15.5	780	7	CO113742
43	122.6	15.5	843	7	CO112338
44	122.2	15.4	578	7	CF507919
45	122	15.4	544	4	BI921995

## ALIGNMENTS

RESULT 1  
CK715561/c  
LOCUS  
DEFINITION  
CK715561 LERSF01B02 Subtractive cDNA library prepared from tomato infected with Ralstonia solanacearum (Rs-CK) Lycopersicon esculentum cDNA clone LERSF01B02, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CK715561  
CK715561.1 GI:50879390  
EST.  
Lycopersicon esculentum (tomato)  
Lycopersicon esculentum

REFERENCE  
AUTHORS  
TITLE  
Lin W.C., Cheng M.L., Ting H.M. and Cheng C.P.  
Functional genomics study of tomato genes responsive to bacterial wilt

JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: Chiu-Ping Cheng  
Crop Plant Improvement Group  
Institute of Bioagricultural Sciences, Academia Sinica  
Nankang, Taipei, 115, Taiwan, Republic of China  
Tel: 886-2-2652-2268  
Fax: 886-2-2561-5600  
Email: chiuping@gate.sinica.edu.tw  
Insert length: 605 Std Error: 0.00  
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Seq primer: Spc.

## FEATURES

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Location/Qualifiers  
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/mol\_type="mRNA"  
/cultiivar="Hawaii7996"  
/db\_xref="taxon:4081"  
/clone="LERSF01B02"  
/feature\_type="root and collar"  
/dev\_stage="Three weeks old"  
/lab\_host="Xil-Blue"  
/note="Vector: pGEM-T-EZ; Plant samples were provided by Dr. Jaw-Fen Wang (Tainan, AYDC). Each plant grown in a 3-inch pot was inoculated with 30 ml (108cfu/ml) of Rs strain Pas4 to give a final concentration of 108cfu/g soil. Roots and collars of inoculated and control plants were harvested 24 and 48 hours post inoculation (e.g.

## ORIGIN

24-control, 24-inoculated, 48-control and 48-inoculated). Poly(A) RNA was purified from total RNA specimen isolated from individual samples. The poly(A) RNA specimen prepared from 24-control and 48-control samples were mixed at 1:1 ratio. The poly(A) RNA specimen prepared from 24-inoculated and 48-inoculated samples were also mixed at 1:1 ratio. Tomato cDNA library LERSF was then constructed by subtracting the pooled control specimen from the pooled inoculated specimen using CLONTECHPCR-select cDNA Subtraction kit."

Query Match 20.3%; Score 161; DB 7; Length 605;  
Best Local Similarity 73.3%; Pred. No. 1.8e-31;  
Matches 206; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 304 GATTGAAACCGGTATAGGGCGTTAGACGGCCGCGTGGGGGAAAGTTCCGGCCGAGATA 363  
DB 343 GATTGAAACCGGTATAGGGCGGTAGACGGCCGCGTGGGGGAAAGTTCCGGCCGAGATA 284  
QY 364 AGGATCCGAAAAAGAAAGATTCAGGATTTGGTGGTACATACGACACCTGAGAT 423  
DB 283 AGAGACCCCGATAGAAAGAGTCTAGGCTTTGGCTAGGACTTACGGACACCTTAAGAT 224  
QY 424 GAGCATTGGCTTATGATGACAGCCGCGTTAAATATCGTGAGCTAAAGCTTAAAT 483  
DB 223 GAGCATTGGCTTATGACAGCCGCGTTAAATATCGTGAGCTTAAAGCTTAAAT 164  
QY 484 TTTTCCTATTGATTTGTTGCAATATTTCCGAGCCCGTAAAGTAAACCCGAGAAAGT 543  
DB 163 TTTTCCTATTGATTTGTTGCAATATTTCCGAGCCCGTAAAGTAAAGTAAAGT 104  
QY 544 TTCCCTGCGAGCGCTTCTACAGAGTGTGCTGCTTCTTCTTC 584  
DB 103 TGCCACTCGTACAGTATCATTTGTAATATACCTTTC 63

RESULT 2  
CN385373 944 bp mRNA linear EST 31-AUG-2004  
LOCUS LE2TR03624 Tomato CL5915 roots under different developmental stages  
DEFINITION Lycopersicon esculentum cDNA clone LE2TR03624, mRNA sequence.  
ACCESSION CN385373  
VERSION CN385373.1 GI:51700687  
KEYWORDS EST.  
SOURCE Lycopersicon esculentum (tomato)  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 944)  
Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.  
DNA microarray profiling of gene expression during tomato root development

JOURNAL COMMENT Unpublished (2004)  
Contact: Kin-Ying, To  
Crop Plant Improvement Group  
Institute of Biagricultural Sciences, Academia Sinica  
128 Academia Rd, Section 2, Taipei, Taiwan 11529

TELE: 886-2-2561-3161  
FAX: 886-2-2561-5600  
Email: kyto@gate.sinica.edu.tw  
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source Location/Qualifiers  
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/organism="Lycopersicon esculentum"  
/mol\_type="mRNA"  
/cultiivar="CL5915"  
/db\_xref="taxon:4081"  
/clone="LE2TR03624"  
/issue\_type="roots"

## ORIGIN

/dev\_stage="1-, 2-, 3-, and 4- month-old"  
/lab\_host="B.coli BM25.8"  
/clone\_lib="Tomato CL5915 roots under different developmental stages"  
/note="Vector: pT7Blue2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-, 2-, 3-, 4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)"

Query Match 19.5%; Score 154.6; DB 7; Length 944;  
Best Local Similarity 70.0%; Pred. No. 9.9e-30;  
Matches 208; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 256 GTTGTGGGAACCCCGCAGAAAGCGCGCGGAGAGAGTTGTCGAAGATTGGAACCGG 315  
DB 229 GTTGAAGATCCAGACAGTGTGGCAAGTGGAAACAGCACCAAAATTTGGAAGCGG 288  
QY 316 TATAAGGCGCTTACAGCGCGCGCGTGGGGAAGTTCCGCGGAGATAAGATCCGAA 375  
DB 289 TACCGAGAGATTAAGAAAGAGAGCGCTGGGTAATTCGCGGAGATAAGATCCGAA 348  
QY 376 AAGAAAGATCCAGATTTGTTGGGTACATACAGACACTGAGATGACGATTTGCT 435  
DB 349 AAGAAATATCGAATTAATGTTAGGACTTATAGACACCGAGATGACGATTTGCT 408  
QY 436 TATGATGACAGCCCGTTTAAATATGCTGAGAGCTAAAGCTTAATTTCTCATTTTG 495  
DB 409 TATGACCAACCCGATTCAGATTTGCTGCTCAAAAGCTAAGGTTAAATTTCTCATTTTA 468  
QY 496 ATTGTTGCAATTTTCCGAGCCGCTTAAAGTAAACCCGAGAAAGCTTCCCTGG 552  
DB 469 ATGCGCTCGGCTGTGCCAGCGCGCTAAGGTGAACCTTAAGGCTGATCGCATTCG 525

RESULT 3  
CN385772 673 bp mRNA linear EST 31-AUG-2004  
LOCUS LE2TR04102 Tomato CL5915 roots under different developmental stages  
DEFINITION Lycopersicon esculentum cDNA clone LE2TR04102, mRNA sequence.  
ACCESSION CN385772  
VERSION CN385772.1 GI:51701086  
KEYWORDS EST.  
SOURCE Lycopersicon esculentum (tomato)  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 673)  
Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.  
DNA microarray profiling of gene expression during tomato root development

JOURNAL COMMENT Unpublished (2004)  
Contact: Kin-Ying, To  
Crop Plant Improvement Group  
Institute of Biagricultural Sciences, Academia Sinica  
128 Academia Rd, Section 2, Taipei, Taiwan 11529

TELE: 886-2-2561-3161  
FAX: 886-2-2561-5600  
Email: kyto@gate.sinica.edu.tw  
Insert Length: 673 Std Error: 0.00  
Plate: 04 row: I column: 02  
Seq primer: smart2.

FEATURES  
source Location/Qualifiers  
1..673

/organism="Lycopersicon esculentum"  
/mol\_type="mRNA"  
/cultiivar="CL5915"  
/db\_xref="taxon:4081"  
/clone="LE2TR04102"  
/issue\_type="roots"

/dev stage="1-2-3", and 4 - month-old"  
 /lab\_host="E.coli BM25.8"  
 /clone\_lib="Tomato CL5915 roots under different developmental stages"  
 /note="Vector: pTriplex2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-2-3-4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)"

## ORIGIN

Query Match 19.3%; Score 153; DB 7; Length 673;  
 Best Local Similarity 69.7%; Pred. No. 2.5e-29; Indels 0; Gaps 0;  
 Matches 207; Conservative 0; Mismatches 90;

256 GTTGTGGAGACCCCGCCAGAGCGCGCGAGAGGTTTCAGAGATTGGAACCG 315  
 193 GTTGAAGAGTCCGAGACAGTGTGCAAGTGAACACGACCAAAAGATTGGAACCG 252  
 316 TATAGAGCGGTTAGACGCGCGCGGAGAGTTCCGCGGAGATAGAGATCCGAAA 375  
 253 TACCGAGAGTAAAGAGAGCGCGGTGGGTAATTCGCGCGAGATAGAGATCCG 312  
 376 AAGAAAGATCCAGATTGTTGGTATACATAGACACCTAGAGATGAGATGGCT 435  
 313 AAAAAAATGCGAGATTATGTATGAGACTTATGAGACACCGAGATGAGATGGCT 372  
 436 TATGATGACAGCGCGGTTTATATGCGTAAAGCTAAGCTAATTTCTCATTTG 495  
 373 TATGACCAAGCCGATTCAGATTCTGTGCTCCAAAGCTAAGCTAATTTCTCATTTA 432  
 496 ATTGATGCAATATTTCCGAGCCGCTTAAAGTAAACCGGAAACGTTTCCCTGCG 552  
 433 ATCGGCTCGGGGTGTGCCGAGCGCGCTAGAGGTAAACCTAGCGTGCATTCG 489

RESULT 4 760 bp mRNA linear EST 19-MAR-2004  
 CK936905  
 LOCUS CGF1004516 G04 Developing fruit flavone at 80 DAFB Citrus sinensis  
 DEFINITION cDNA F800AB0002\_IIIF\_G04 5', mRNA sequence.  
 ACCESSION CK936905  
 VERSION CK936905.1 GI:45450103  
 KEYWORDS EST.  
 SOURCE Citrus sinensis  
 ORGANISM Citrus sinensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eustosids II; Sapindales; Rutaceae; Citrus.  
 1 (bases 1 to 760)  
 Uratcu,S., Baek,J., Leslie,A., Xu,J., Cook,D., and Dandekar,A.  
 Analysis of peel specific genes in Citrus (2004)  
 Unpublished (2004)  
 Contact: Abhaya Dandekar, PhD  
 CAES Genome Facility  
 UC Davis, Department of Pomology  
 One Shields Ave, Davis, CA 95616, USA  
 Tel: 530 752 7784  
 Fax: 530 752 8502  
 Email: amdandekar@ucdavis.edu  
 Seg primer: WSC-F-TCCGAGATCTGACGACGAC.  
 Location/Qualifiers  
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REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
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 /organism="Citrus sinensis"  
 /mol\_type="mRNA"  
 /cultivar="Washington navel orange"  
 /db\_xref="taxon:2711"  
 /clone="F800AB0002\_IIIF\_G04"  
 /sex="Hermaphrodite"  
 /cell\_type="Palvedo"  
 /dev\_stage="Developing fruit sample-collected July 29, 2003"

/lab host="X110-Gold"  
 /clone\_lib="Developing fruit Flavado at 80 DAFB"  
 /note="Torgan: Fruit; Vector: pTriplex2; Site 1: 5f11A; Site 2: 5f11B; Developing citrus fruits were harvested from trees growing in the 'Citrus variety collection' in the Wolfekill experimental orchard located in Winters, California (USA). Fruit was collected on July 29, 2003, between 8 to 9 am and stored at 4C. The flavado tissue was dissected out of developing fruit (80 DAFB) and used to isolate RNA using Trizol reagent from Invitrogen. The cDNA library was constructed using the SMART cDNA library kit (Clontech). The primary library was en masse evicted and plasmid DNA containing the cDNA library was isolated from the resultant bacterial population. Plasmid DNA was then transformed into ultra competent E coli cells (X110 Gold, Stratagene). Transformants were plated out on Q-trays (2000 cfu/tray), picked using a Qbot and archived in 384 well dishes."

## ORIGIN

Query Match 19.2%; Score 152.4; DB 7; Length 760;  
 Best Local Similarity 67.8%; Pred. No. 3.6e-29; Indels 0; Gaps 0;  
 Matches 213; Conservative 0; Mismatches 101;

282 GGCCGAGAGGTTGTTGAGAGATTGAAACCGGTATAGGGCGGTAGACGGCGCGT 341  
 278 GATGTGGACGCGGACTCAGTGAGTGAAGTGAAGCGGTGAGAGAGCGCGT 337  
 342 GGGGAAGTTCCGCGCGAGATAGGATCCGAAAAAGAAAGATCCAGATTGTTGG 401  
 338 GGGGAAGTTGCTGCGGAGATAGAGGACCTTAAGAAAGATGGGGCAAGATTGGCTGG 397  
 402 TACATACGACACTGAGAGTGCAGATTGCTTATGATGACGCCGCTTATATATGCG 461  
 398 CACCTATGATACCCCGAGGGTGCAAGTTCCTATGATGAGCCGCTTCAAGATGCG 457  
 462 TGGAGTAAAGTAGGCTTAATTTCCATTTGATGTTGATGATATTCGGAGACCGGT 521  
 458 AGGCTTCAAGGCTTACCTCAATTTCTCACTCATGCTCAAAAGTTGAGCCCGGT 517  
 522 TAGATTAACCCGAGAAACGTTTCCCTCGAGACCTTTCAGACCTGCTGCTTCTTC 581  
 518 TAGGTTACCAAGAACCGGTGCTTCCAGAGCTCTCTCTGCTTCTTCTTCTTC 577  
 582 TTCTTCTGCTG 595  
 578 ATCATCATCCGTTG 591

RESULT 5 903 bp mRNA linear HTC 06-FEB-2004  
 CNS0A88X  
 LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone GS19S1L772E09 of Silique of strain col-0 of Arabidopsis thaliana (thale cress).  
 DEFINITION  
 ACCESSION CNS0A88X  
 VERSION BX821822.1 GI:42467265  
 KEYWORDS HTC; GSLT cDNA.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 903)  
 Castelli,V., Aury,J.M., Jallion,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Querier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.  
 Whole Genome Sequence Comparisons and 'Full-length cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation  
 Unpublished  
 2 (bases 1 to 903)  
 Genoscope.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 Genoscope.

TITLE Direct Submission  
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castel J.V., Aury J.M., Jallion O., Winkler P., Menard M., Craud C., Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information Center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full\_length  
http://www.genoscope.cns.fr/cgi-bin/gsb/gsb?source=Arabidopsis.

FEATURES  
source  
location/Qualifiers  
1..903  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/strain="Col-0"  
/db\_xref="taxon:3702"  
/clone="GSLTSL77ZE09"  
/issue\_type="Siliques"  
/plasmid="pCMVSPORT\_6"  
1..903  
/gene="At2g44840"

ORIGIN  
Query Match 16.8%; Score 134; DB 3; Length 903;  
Best Local Similarity 63.8%; Pred. No. 2.8e-24;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 233 CGAAGACGTCTGACGAGATTCCTGTTGGGAACCCCGCAGAACCGCGCCGAGAG 292  
DB 276 CCGTACCTCTCCGCGGAGGAAATPAACCTCCGCGACGAAAGGAGTGGCTCACAG 335  
QY 293 GTTGTTGAGAGATTGGAACCGGTATAGGGCGTTAGACGCGCGCGTGGGAGAGTTG 352  
DB 336 CGCCGAGGAGAAAGGGAGTGCAGTACAGAGAGTGAAGAGCGCCGTGGGAAATTG 395  
QY 353 CGCGGAGATTAAGGATTCGAAAAGAAAGATCCAGATTTGGTGGTACATACAGA 412  
DB 396 CGCGGAGATTAGGATCCGAAAGAAAGAGAGCTAGGGTTGGCTCGGAGCTTACAGA 455  
QY 413 CACCTGAGATGACGATTTGGCTTATGATGACCGCCGTTTAAATATGCTGAGCTAAG 472  
DB 456 CGCGGAGAGCGCGGGTGGCGTACGACCGCGCGTTTCACTCAGAGGATGAAAG 515  
QY 473 CTAGGCTTAATTTTCTCATTTGATTGTTGCAATATTTCCGAGCCCGTTAGATAAC 532  
DB 516 CTAGCTGAATTTTCCGCAATTGATTGTTCTTGAATAGATGACCGGTTAGATTAGC 575

QY 533 CGAAGAAACGTTCCCTG 550  
DB 576 CTCGCGCTCGCTCGCCG 593

RESULT 6  
AV552445 563 bp mRNA linear EST 23-FEB-2004  
LOCUS AV552445 Arabidopsis thaliana roots Columbia Arabidopsis thaliana  
DEFINITION CDNA clone R22h02R 5', mRNA sequence.  
ACCESSION AV552445  
VERSION AV552445.1 GI:8723858  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1 (bases 1 to 563)

AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

COMMENT JOURNAL DNA Res. 7 (3), 175-180 (2000)  
MEDLINE 20363093  
PubMed 10907847  
Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizukazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES  
source  
location/Qualifiers  
1..563  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/db\_xref="R22h02R"  
/issue\_type="roots"  
/clone\_lib="Arabidopsis thaliana roots Columbia"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
Query Match 16.8%; Score 133; DB 1; Length 563;  
Best Local Similarity 65.1%; Pred. No. 4.6e-24;  
Matches 196; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 233 CGAAGACGTCTGACGAGATTCCTGTTGGGAACCCCGCAGAAAGCGGCGCAGAGAG 292  
DB 260 CCGTACCTCTCCGCGGAGGAAATPAACCTCCGCGACGAAAGGAGTGGCTCACAG 319  
QY 293 GTTGTTGAGAGATTGGAACCGGTATAGGGCGTTAGACGCGCGCGTGGGAGAGTTG 352  
DB 320 CGCCGAGGAGAAAGGGAGTGCAGTACAGAGAGTGAAGAGCGCCGTGGGAAATTG 379  
QY 353 CGCGGAGATTAAGGATTCGAAAAGAAAGATCCAGATTTGGTGGTACATACAGA 412  
DB 380 CGCGGAGATTAGGATCCGAAAGAAAGAGAGCTAGGGTTGGCTCGGAGCTTACAGA 439  
QY 413 CACCTGAGATGACGATTTGGCTTATGATGACCGCCGTTTAAATATGCTGAGCTAAG 472  
DB 440 CGCGGAGAGCGCGGGTGGCGTACGACCGCGCGTTTCACTCAGAGGATGAAAG 499  
QY 473 CTAGGCTTAATTTTCTCATTTGATTGTTGCAATATTTCCGAGCCCGTTAGATAAC 532  
DB 500 CTAGCTGAATTTTCCGCAATTGATTGTTCTTGAATAGATGACCGGTTAGATTAGC 559

QY 533 C 533  
DB 560 C 560

RESULT 7  
BE449392 591 bp mRNA linear EST 18-MAY-2001  
LOCUS BE449392  
DEFINITION EST356151 L. hirsutum trichome, Cornell University Lycopersicon  
ACCESSION BE449392  
VERSION BE449392.1 GI:9454895  
KEYWORDS EST.  
SOURCE Lycopersicon hirsutum (Solanum hirsutum)  
ORGANISM Lycopersicon hirsutum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE  
AUTHORS van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Romling, C.M., Niernan, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.  
Generation of ESTs from wild tomato (Lycopersicon hirsutum)

TITLE

Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Qy	233	CGAAGAGCTGTCAAGAGGATTTCTGTGTGGAAACCCCGCAGAAACCGCGCCCGAGAG	292
Db	291	CGGTAACTCTCCGGCGGAAGAAATAAGCTCCCGGCGAGCGAAGGCGAATGGCTCACACG	350
Qy	293	GTTTGTTGAAAGATTGGAACCGGTATTAAGGCGCTTAAACGGCGGCTCTGGGGGAATTCG	352
Db	351	CGCGGAGCGAAGGGGATGCACTATCAAGAAAGTGAAGAAAGAGGCTGTGGGGGAAATTCG	410
Qy	353	CGCGGAGATTAAGGATCCGAAAGAAAGAAAGATCCAGATTTGGTTGGTATCATACGAA	412
Db	411	CGCGGAGATTAAAGATCCGAAGAAAGAGAGCTAAGGTTGGCTCGGGACTTACGAA	470
Qy	413	CACCTGAGATGACGACTTGGCTTAATGATGACGCGCGTTTAATATGCGTGGAGCTAAAG	472
Db	471	CGCGGAGGACGGCGCGGTGGCGTACACACGAGCGGGGTTTCAGCTAGAGAGATCGAAAG	530
Qy	473	CTAAGCTAATTTTCCATCTTATGATGGTTCGAATATTTCCGGAACCGGTTAGAGTAAAC	532
Db	531	CTAAGCGAATTTTCCGCAATTTGATGGTTCTTGAATATGAGCCGCGTTAGATTAGGC	590
Qy	533	C 533	
Db	591	C 591	

Contact: Dohi Choi  
Genome Research Center and National Center for Genome Information  
Korea Research Institute of Bioscience and Biotechnology  
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea

Tel: 82-42-860-4340  
 Fax: 82-42-860-4309  
 Email: doi@mail.krdb.re.kr  
 Plate: 018 row: B column: 10.

## FEATURES

Location/Qualifiers

1. 490

/organism="Capsicum annuum"

/mol\_type="mRNA"

/db\_xref="taxon:4072"

/clone\_lib="KS11"

## ORIGIN

Query Match 16.8%; Score 132.8; DB 6; Length 490;  
 Best Local Similarity 67.1%; Pred. No. 5.1e-24;  
 Matches 188; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 305 ATTGGAACCGGTATTAAGGCGCTTAAAGCGCGCGCGTGGGGAAGTTCCGGCGGAGATTA 364  
 DB 179 ATAGGAGAGATACATAGAGGCTGAGCGGAGCAATGGGGTACGTTTCTGAGAGATTA 238  
 QY 365 GGGATCCGAAAAAGAAAGATCCAGATTGGTGGGTACATACGAGACACCTGAGATG 424  
 DB 239 GAGATCCGAAATAGAGAGCGCGAGGCTATGGCTAGGAATTATGAGACTCCTGAGGATG 298  
 QY 425 CAGCATTTGGCTTATGATGACCGCGCTTAAATATGCGTAGCTAAAGCTAGGCTTAAT 484  
 DB 299 CAGCATTTGGCTTATGACCAAGCGCATTCATAAATTCGTGGCTGAAAGCTCGGCTCAAT 358  
 QY 485 TTCCCTATTGATTGTTGTAATTTCCGGAACCGCTTAGATAAACCGGAAAAACGTT 544  
 DB 359 TTCTTAATTTGATGAGCTCGGAGTGGCTGATGACTAACCGTAGAGCCCGTA 418  
 QY 545 TCCCTGCGAGCGCTTACGAGCTGCTGCTTCTTCTTC 584  
 DB 419 CGGATCGCCCGGAGCATGACTTCTCTCTGATCATC 458

## RESULT 10

CB078370

LOCUS

DEFINITION

h66g10.g1 Hedycotis terminalis flower - Stage 2 (NYBG)

CB078370

VERSION

KEYWORDS

SOURCE

ORGANISM

Hedycotis terminalis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Gentianales; Rubiaceae; Rubioideae; Spermaceae; Hedycotis.

1 (bases 1 to 636)

Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhi, N.N., O'Shaughnessy, A.L., Ballja, V., Martienssen, R.A., McCombie, R.W., Bentley, P. and Stevenson, D.

Expressed tag sequences from Hedycotis terminalis flower - Stage 2 (NYBG)

JOURNAL

COMMENT

Unpublished (2003)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mccombie@cshl.org

Plate: h66 row: 9 column: 10

Seq primer: -21M3UnivRev

High quality sequence stop: 636.

Location/Qualifiers

1. 636

/organism="Hedycotis terminalis"

/mol\_type="mRNA"

/db\_xref="taxon:219667"

/clone="h66g10"  
 /dev stage="pre-anthesis; Stage 2"  
 /clone\_lib="Hedycotis terminalis flower - Stage 2 (NYBG)"  
 /note="Organ: flower; Vector: pAK-CMV; Site 1: XhoI; Site 2: Eco RI; Date: Completed 12/18/01. Submitted to SHU 12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii; NYBG herbarium voucher TW2562"

## ORIGIN

Query Match 16.7%; Score 132.6; DB 6; Length 636;  
 Best Local Similarity 69.5%; Pred. No. 6e-24;  
 Matches 180; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 245 AGGAGATTCTGTGTGGGAAACCCCGCCAGAGCGGCGCGGAGGAGTGTTCGAAG 304  
 DB 281 AGAGGTACAGCAAGATGTTCCGCGCGCGCGCGAGTGGAAACACTGATACG 340  
 QY 305 ATTGGAACCGGTATTAAGGCGCTTAAAGCGCGCGTGGGGAAGTTCCGGCGGAGATTA 364  
 DB 341 AGTGAAGCGCATACAAAGTGTTCGAGAGAGCGCGTGGGGAAGTTCCGGCGGAGATTA 400  
 QY 365 GGGATCCGAAAAAGAAAGATCCAGATTGGTGGTACATACGACACCTGAGATG 424  
 DB 401 GAAACCCGGGGAAGAAAGATCCAGAAATATGCTGGGAACTGACGAGACCGGAGATG 460  
 QY 425 CAGCATTTGGCTTATGATGACCGCGCTTAAATATGCTGAGGCTAAAGCTTAGCTTAAT 484  
 DB 461 CGCATTTGGCTTACGACCGCGCGCTTACCACTGAGGAGTGGAAAGCTTAGCTTAAT 520  
 QY 485 TTCTCATTTGATTGTTTC 503  
 DB 521 TTCCACATATGATTGATC 539

## RESULT 11

BF275652

LOCUS

DEFINITION

GA\_Eb0024J23f Gossypium arboreum 7-10 dpa fiber library Gossypium

arboreum cDNA clone GA\_Eb0024J23f, mRNA sequence.

BF275652

VERSION

KEYWORDS

SOURCE

ORGANISM

Gossypium arboreum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

1 (bases 1 to 903)

Wing, R.A., Fritch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

Unpublished (2000)

Contact: Wing RA

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: twing@clemson.edu

Seq primer: TAATACGACTCACTATAGG

High quality sequence start: 48

High quality sequence stop: 683.

Location/Qualifiers

1. 903

/organism="Gossypium arboreum"

/mol\_type="mRNA"

/strain="AKA"

/cultivar="B400"

/db\_xref="taxon:29729"

/clone="GA\_Eb0024J23f"

## ORIGIN

/tissue\_type="Fibers isolated from bolls harvested 7-10  
dpa"  
/lab\_host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBR-CMV; Site\_1: EcoRI; Site\_2: XhoI"

Query Match 16.4%; Score 130.2; DB 2; Length 903;

Best Local Similarity 66.7%; Pred. No. 2.8e-23;

Matches 186; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 316 TATAGAGGCGCTTACGAGCGCGCGCGGAGGAGTTCGCGCGAGATAGAGATCCGAA 375  
Db 178 TAGAGGGAGTAGAGAGAGGCGCGCGAGCATACCGAGATAGAGATCCGAA 237  
QY 376 AAGAAAGATCCAGATTTGGTGGTACATACGAGACACCTAGAGATGAGCATTTGGT 435  
Db 238 CGAAACGGTGCAGAGATCTGGCTCGGTACTTACGAGACTCCGAGGGTCTGGCGTACT 297  
QY 436 TAGATGACGCGCGCTTATATGCGTGGAGCTTAAAGCTTATTTCTCATTTG 495  
Db 298 TACGACAGAGCGCGCTTATATGCGTGGAGAGAGCTGAAATTTTCCCACTC 357  
QY 496 ATGCTTCGAAATTTCCGAGACCGCTTACGATTAACCCGAGAAACGTTCCCTGCGAG 555  
Db 358 ATCGCTCGATCAGGAGGAGCGCGTGAAGTACGATTAACGAGAAATCCCTGAA 417  
QY 556 CTTTCTACGACGTCGTCT 594  
Db 418 ACGTCT 456

## RESULT 12

LOCUS BG128566 652 bp mRNA linear EST 31-JAN-2001  
DEFINITION EST474212 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
CTOP214 5' sequence, mRNA sequence.

ACCESSION BG128566  
VERSION BG128566.1 GI:12628754  
KEYWORDS EST.  
SOURCE Lycopersicon esculentum (tomato)  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 652)  
AUTHORS van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Uterback, T.,  
Hansen, C., Roming, C. and Tankesley, S.  
Generation of ESTs from tomato shoot/meristem tissue  
Unpublished (2001)  
TITLE Clemson University Genomics Institute  
JOURNAL Contact: CUGI  
COMMENT Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.

## FEATURES

source location/Qualifiers

1..652  
/organism="Lycopersicon esculentum"  
/mol\_type="mRNA"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone\_lib="CTOP214"  
/tissue\_type="shoot/meristem"  
/dev\_stage="developing shoots from 4-6wks old plants"  
/lab\_host="SOLR"  
/clone\_lib="tomato shoot/meristem"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Small expanding leaves from the growing tip were  
taken from greenhouse plants (4-6wks old TA496). Tissue  
was immediately frozen in liquid nitrogen."

## ORIGIN

Query Match 16.4%; Score 129.8; DB 4; Length 652;

Best Local Similarity 65.2%; Pred. No. 3.3e-23;

Matches 191; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 278 CGCGCCCGAGAGAGGTTGTTGAGAGATTGGAACCGGATTAAGCGCGCGC 337  
Db 124 CGGACAGCTCCGCGGCTGAAACCCGAAAGAGAGATTATAGCGCTTAGCACGCTC 183  
QY 338 CGTGGGGGGAAGTTCGCGGCGAGATTAAGGATCCGAAAGAAAGATCCAGATTGGT 397  
Db 184 CGTGGGGGGAAGTTCGCGGCGAGATTAGAGATCCGCGAAAGAGAGCTTAGGGTTGGC 243  
QY 398 TGGGTACATACGAGACCTGAGATGACATTTGGCTTATATGAGCGCGCTTAAATA 457  
Db 244 TTGGAACGTACGAAACAGCTGAGAGAGCTGATTTGCTTATATAGTCTTATAGAA 303  
QY 458 TGGGTGAGCTAAAGCTTAAATTTCTTCATTTGATTTGGTTGCAATATTTCCGAC 517  
Db 304 TGAGAGATCAAAAGACATTTGAAATTTCCCGACCGGATCGGTTGAATGAACCGGAC 363  
QY 518 CGGTTAGATTAACCCGAGAAACGTTTCCCTGCGAGCTTTACGAGCTCG 570  
Db 364 CGGTTGAGATTACGCGGAAAGGCGAGATCGCCGAGACCGGACCTGCTG 416

## RESULT 13

LOCUS A1771213 437 bp mRNA linear EST 18-MAY-2001  
DEFINITION EST252409 tomato ovary, TAMU Lycopersicon esculentum cDNA clone  
CLE2D29K9, mRNA sequence.

ACCESSION A1771213  
VERSION A1771213.1 GI:5269350  
KEYWORDS EST.  
SOURCE Lycopersicon esculentum (tomato)  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 437)  
AUTHORS Alcalá, J., Vrebalov, V., White, R., Matern, A.L., Vision, T.,  
Holt, I.E., Liang, F., Upton, J., Roming, C.M., Craven, M.B.,  
Fujii, C.Y., Bowman, C.L., Niernan, W., Fraser, C.M., Venter, D.C.,  
Martin, G.B., Tankesley, S.D. and Giovannoni, J.  
Generation of ESTs from tomato carpel tissue  
Unpublished (1999)  
TITLE Clemson University Genomics Institute  
JOURNAL Contact: CUGI  
COMMENT Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

## FEATURES

source location/Qualifiers

1..437  
/organism="Lycopersicon esculentum"  
/mol\_type="mRNA"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone\_lib="CLE2D29K9"  
/tissue\_type="carpel"  
/dev\_stage="5 days pre-anthesis to 5 days post-anthesis"  
/lab\_host="X11-Blue MRP"  
/clone\_lib="tomato ovary, TAMU"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; cLBD - Tomato Carpel EST library. OligoDT-primed and  
directionally cloned cDNA in vector Lambda Zap II with 5'  
and 3' ends located at the EcoRI and XhoI sites,  
respectively."

## ORIGIN

Query Match 16.2%; Score 128.6; DB 1; Length 437;

Best Local Similarity 69.0%; Pred. No. 6.4e-23;

Matches 176; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 316 TATAGGCGCTTACGAGCGCGCGGAGGAGTTCGCGCGAGATAGAGATCCGAA 375

Db 10 TATAGAGGCGTTAGACAGCGTCCTGCGGGGAAATTTGCGCGAGATTAGAGATCCGGCG 69  
 Qy 376 AAGAAAGATCCAGATTTGTTGGGTATACATACGAGACCTGAGGATGACAGATTGCT 435  
 Db 70 AAGACCGAGCTTGGGTTGGCTTGGAGCTGACGAAACGCTGAAAGAGCTCAATTGCT 129  
 Qy 436 TATGATGACCGCGCTTATATATGCGTGAGCTAAAGCTTAAATTTTCTCATTTG 495  
 Db 130 TATGATTAAGCTCTTATGAAATGAGAGATCAAAAGCATTGTAATTTCCGACCGG 189  
 Qy 496 ATTGTTTCCAAATTTTCCGAGCCCTTAAAGTAAACCGAGAAAACGTTTCCCTGCGAG 555  
 Db 190 ATCGATTGAAATTAACCGAGACCGGTTGAGATTACCGGAAAGGCGAGCATGCGCGAA 249  
 Qy 556 CCTTACGACGCTG 570  
 Db 250 CCGGCAAGCTCGTCG 264

RESULT 14  
 AM034216 575 bp mRNA linear EST 18-MAY-2001  
 LOCUS EST277787 tomato callus, TAMU Lycopersicon esculentum cDNA clone  
 DEFINITION CLEC32P18 similar to Pti4, mRNA sequence.  
 ACCESSION AM034216  
 VERSION AM034216.1 GI:5892972  
 KEYWORDS EST.  
 SOURCE Lycopersicon esculentum (tomato)  
 ORGANISM Lycopersicon esculentum

REFERENCE  
 AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upson, J., Craven, M.B., Bowman, C.L., Ahn, S., Romling, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.  
 TITLE Generation of ESTs from tomato callus tissue  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.

## FEATURES

## Source

1..575  
 Location/Qualifiers  
 /organism="Lycopersicon esculentum"  
 /mol\_type="mRNA"  
 /cultivar="TA96"  
 /db\_xref="taxon:4081"  
 /clone="CLEC32P18"  
 /issue\_type="callus"  
 /dev\_stage="25-40 days old"  
 /lab\_host="Xl1-Blue MRF"  
 /clone\_lib="tomato callus, TAMU"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Giovannoni laboratory; CLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST library"

## ORIGIN

Query Match 16.2%; Score 128.2; DB 2; Length 575;  
 Best Local Similarity 64.8%; Pred. No. 8.6e-23;  
 Matches 190; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 278 CCGCGCGCGAGAGATTGTTCGAAGATTGAAACCGGATTAAGCGCTTAACCGCGCG 337  
 Db 278 CCGCGACCTCCGCGCGGTGAACACCGAAGGAGAGACATTATGAGCGCTTACAGCGCTC 337

Qy 338 CGTGGGGGAATGTCGCGCGAGATTAAGGATCCGAAAAAGAGATCCAGATTGCT 397  
 Db 338 CGTGGGGGAATTTGCGCGCGAGATTAAGATCCGCGAAGAGAGAGCTAGGTTGCGC 397  
 Qy 398 TGGGTACATCGAGACACCGAGATGACGATTTGGCTTATATGAGCGCGTTAAAT 457  
 Db 398 TTGGAACGTACGAAACGCTGAAAGAGCTGCAATTCCTTATGATTAAGCTGCTATAGAA 457  
 Qy 458 TGCCTGAGCTAAAGCTTAAATTTCTCATTTGATTTGATTCGAATATTTCCGAGC 517  
 Db 458 TGAGAGATCAAAAGCAGCATTTGATTTCCCGACCGGATCGTTGATGAAACCGGAA 517  
 Qy 518 CCGTTAGATTAACCGGAGAAACGTTTCCCTGCGAGCTTCTACAGCTG 570  
 Db 518 CCGTTGAGATTACGCGGAAAGCGAGCATCCGCGAACCAGCAAGCTGCTG 570

RESULT 15  
 AM584731 638 bp mRNA linear EST 07-SEP-2000  
 LOCUS N210846e MHAM Medicago truncatula/Gloms versiforme mixed EST  
 DEFINITION library cDNA clone MHAM-7M11, mRNA sequence.  
 ACCESSION AM584731  
 VERSION AM584731.1 GI:7261785  
 KEYWORDS EST.  
 SOURCE Medicago truncatula/Gloms versiforme mixed EST library  
 ORGANISM Medicago truncatula/Gloms versiforme

REFERENCE  
 AUTHORS Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.  
 TITLE ESTs from roots of Medicago truncatula after colonization with Gloms versiforme  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Harrison M.J.  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73401  
 Tel: 580-223-5810  
 Fax: 580-221-7380  
 Email: [mj.harrison@noble.org](mailto:mj.harrison@noble.org)  
 Other name: MHAM-7a-G06; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at '<http://chryslie.tamu.edu/medicago>'.  
 Seq primer: T3.

## FEATURES

## Source

1..638  
 Location/Qualifiers  
 /organism="Medicago truncatula/Gloms versiforme mixed EST library"  
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 /cultivar="Medicago truncatula genotype A17"  
 /db\_xref="taxon:119092"  
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 /issue\_type="roots colonized with Gloms versiforme"  
 /dev\_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Gloms versiforme. The library was made from a mixture of RNA from each of these stages."  
 /lab\_host="E. coli strain XL0LR"  
 /clone\_lib="MHAM"  
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Gloms versiforme. The cDNA was directionally ligated into the unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-aseIst helper phage and propagated in XL0LR cells."

## ORIGIN

Query Match 16.2%; Score 128; DB 2; Length 638;  
 Best Local Similarity 73.2%; Pred. No. 9.9e-23;  
 Matches 164; Conservative 0; Mismatches 60; Indels 0; Gaps 0;



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QY 367 GATCCGAAAAAAGAAAGATCCAGGATTGGTTGGGTACATACGAGACACTGAGAGATGA 426
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QY 427 GCATTGGCTTATGATGACGCGCGTTTAAATATGCGTGAAGCTAAAGCTTAAGCTTAATTT 486
Db 356 GCTTGGCTTACGCAAAAGCTGCTTTAAGATGCGTGGCCGAAAGGCCAAAGCTTAATTT 415
QY 487 CCTCATTTGATTGGTTGGAATATTTCCGACCCGTTAGATPAA 530
Db 416 CCCCACTCAITGGCTGTGATGTGTTACACGAGGCCAGAGAA 459

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Search completed: March 7, 2005, 19:12:35  
 Job time : 3392 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2005, 22:06:55 ; Search time 165 Seconds  
(without alignments)  
475.832 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 203  
Sequence: 1 MEEETISVSDRFLSLIEH.....SSSSSSSSSSSGCKRRY 203

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	203	100.0	203	3	AAy97228
2	19	9.4	183	3	AAg24801
3	19	9.4	183	3	AAg34782
4	19	9.4	202	8	ADm72373
5	19	9.4	202	8	ADm72375
6	19	9.4	212	3	AAg24800
7	19	9.4	212	3	AAg34781
8	19	9.4	226	3	AAg34780
9	19	9.4	226	4	AAE02464
10	19	9.4	226	7	ADe37189
11	19	9.4	226	8	ADm1615
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13	19	9.4	226	8	ADm1615
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15	18	8.9	210	3	AAy97227
16	17	8.4	69	2	AAy31467
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18	17	8.4	124	8	ADi43274
19	17	8.4	124	8	ADm63662
20	17	8.4	135	3	AAg09838
21	17	8.4	138	8	ADm63752
22	17	8.4	139	5	AAU92965
23	17	8.4	139	7	ADm30138
24	17	8.4	139	7	ADm37107
25	17	8.4	139	8	ADi41869

26	17	8.4	139	8	ADm61811	Ado61811 Transcrip
27	17	8.4	139	8	ADm62997	Ado62997 Transcrip
28	17	8.4	201	4	AAE02540	AAE02540 A. thalia
29	17	8.4	201	4	ADm30756	Adm30756 Plant Yle
30	17	8.4	201	8	ADi43767	Adi43767 Plant tra
31	17	8.4	201	8	ADm01637	Adm01637 Thalecres
32	17	8.4	201	8	ADm03313	Adm03313 Thalecres
33	17	8.4	201	8	ADm02889	Adm02889 Transcrip
34	17	8.4	207	4	AAE02554	AAE02554 A. thalia
35	17	8.4	207	4	ADm55696	Adm55696 Thalecres
36	17	8.4	207	8	ADm01641	Adm01641 Transcrip
37	17	8.4	207	8	ADm01543	Adm01543 Transcrip
38	17	8.4	282	8	ADi42040	Adi42040 Plant tra
39	17	8.4	282	8	ADi42694	Adi42694 Plant tra
40	17	8.4	299	8	ADm02947	Adm02947 Thalecres
41	16	7.9	131	8	ADi43273	Adi43273 Plant tra
42	16	7.9	131	8	ADm63660	Adm63660 Transcrip
43	16	7.9	173	3	AAG09634	AAg09634 Arabidops
44	16	7.9	173	3	AAG50952	AAg50952 Arabidops
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#### ALIGNMENTS

RESULT 1  
ID AAy97228 standard; protein; 203 AA.  
XX  
AC AAy97228;  
XX  
DT 19-DEC-2000 (first entry)  
XX  
DE Plant transcription factor AP2 DNA-binding domain polypeptide.  
XX  
XX

AP2: transcription factor; plant metabolism; metabolite; primary;  
KW secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;  
KW food colouring; flavouring; fragrance; antimicrobial; pathogenic;  
KW insecticide; gene expression; modulation.  
XX  
XX

OS Catharanthus roseus.  
XX  
PN W0200046383-A2.  
XX  
PD 10-AUG-2000.  
XX  
PF 07-FEB-2000; 2000MO-NL000075.  
XX

PR 05-FEB-1999; 99DK-00000158.  
PR 10-FEB-1999; 99US-0115388P.  
XX  
PA (UYLE-) RIJXSUNIV LEIDEN.  
XX

PI Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;  
XX WPI; 2000-499380/44.  
DR N-PSDB; AAA53745.  
XX

PT Modulating level of metabolites and stress resistance in recombinant  
PT cells for synthesis of plant metabolites such as alkaloids including  
PT terpenoid indole alkaloids, by providing transcription factor to the  
PT cell.  
XX

XX Disclosure; Page 97-98; 101pp; English.

CC Many plant secondary metabolites have value as pharmaceuticals, food  
CC colourings, flavours and fragrances. Some plant secondary metabolites are  
CC linked to plant or plant cell defence mechanisms and may confer to the  
CC plant antimicrobial activity, protection against UV light, herbivores,  
CC pathogens, insects and nematodes. Plant secondary metabolites such as  
CC terpenoid indole alkaloids (TIA) represent a class of pharmaceuticals  
CC useful compounds which naturally occur in many plant species. New methods  
CC are described which modulate the expression of one or more genes involved

CC in the biosynthesis of plant metabolites or their precursors in plant  
CC cells. The method comprises inserting into a plant cell a sequence  
CC encoding a transcription factor comprising an AP2 DNA-binding domain and  
CC by modifying the expression of that transcription factor. Transcription  
CC factors comprising an AP2 DNA-binding domain are useful as central  
CC regulators of complex metabolite pathways involving numerous target genes  
CC for such transcription factors. This means that the yield of commercially  
CC valuable metabolite compounds can be enhanced and the tolerance of plants  
CC towards exogenous stress factors can be influenced. The method is useful  
CC for modulating the level of one or more metabolites. By providing a  
CC transcription factor to the cell the level of the metabolite is enhanced  
CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to  
CC a cell to which the transcription factor is not provided  
CC  
XX  
SQ Sequence 203 AA;

Query Match 100.0%; Score 203; DB 3; Length 203;  
Best Local Similarity 100.0%; Pred. No. 1,5e-181;  
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PSSESCQSNMAESCQEDSVGTTPPAAGCGCKDMNRYKGVRRRPMGKFAEIRDPK 120  
Db 61 PSSESCQSNMAESCQEDSVGTTPPAAGCGCKDMNRYKGVRRRPMGKFAEIRDPK 120  
QY 121 KGSRIWLGTYETPEDAALAYDAAEFMRGAKARLNPPLIGSNISGPRVVRKPPAP 180  
Db 121 KGSRIWLGTYETPEDAALAYDAAEFMRGAKARLNPPLIGSNISGPRVVRKPPAP 180  
QY 181 STTSSSSSSSSSENSGKRRKRY 203  
Db 181 STTSSSSSSSSSENSGKRRKRY 203

RESULT 2  
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ID AAG24801 standard; protein; 183 AA.

XX AC AAG24801;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 28613.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

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Query Match 9.4%; Score 19; DB 3; Length 183;  
Best Local Similarity 100.0%; Pred. No. 2.5e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPWGKFAAIRDPKK 120  
Db 51 GVRRRPWGKFAAIRDPKK 69

## RESULT 3

AAAG34782  
ID AAAG34782 standard; protein; 183 AA.

XX AC  
XX AAAG34782;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 42377.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KM hybridisation assay; genetic mapping; gene expression control; promoter;

XX KM termination sequence.

OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-01231825P.

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PR	20-MAY-1999;	99US-0135124P.
PR	21-MAY-1999;	99US-0135353P.
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Query Match 9.4%; Score 19; DB 3; Length 183;  
Best Local Similarity 100.0%; Pred. No. 2.5e-09;  
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DB 51 GVARRRPWGKFAAETIRDPKK 69

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ID ADM72373 standard; protein; 202 AA.  
AC ADM72373;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Soybean NRTF1c polypeptide.  
XX  
KW Plant; nematode-regulated polypeptide; calcium dependent protein kinase;  
KW CDPK; nematode-responsive transcription factor 1; NRTF1;  
KW nematode-responsive protein; NRP; caffeic acid 7-O-methyltransferase;  
KW 7OM; inositol 5-phosphatase; IPP; nematocidal; gene therapy;  
KW nematode resistance; soybean; enzyme; NRTF1c.  
XX  
OS Glycine max.  
XX  
PN WO2004029222-A2.  
XX  
PD 08-APR-2004.  
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PF 30-SEP-2003; 2003WO-US031029.  
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PR 30-SEP-2002; 2002US-0414771P.  
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PS (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Hu X, Lu G;  
XX  
DR WPI; 2004-316104/29.  
XX  
DR N-PSDB; ADM72372.  
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PT New isolated nucleic acid molecules encoding nematode-responsive  
PT proteins, useful for conferring or improving nematode resistance in  
PT plants.  
XX  
PS Claim 26; SEQ ID NO 11; 143pp; English.  
XX  
CC The invention relates to pathogen-responsive genes that encode a nematode  
CC -regulated polypeptides. The proteins of the invention include calcium  
CC dependent protein kinase (CDPK), nematode-responsive transcription factor  
CC 1 (NRTF1), nematode-responsive protein (NRP), caffeic acid 7-O-  
CC methyltransferase (7OM) or inositol 5-phosphatase (IPP) polypeptides. The  
CC nucleic acid molecule encoding the polypeptides are operably linked to a  
CC promoter that drives expression in a host cell. The composition and  
CC methods are useful for conferring or improving nematode resistance in  
CC plants. The present sequence represents a soybean NRTF1c polypeptide.  
XX  
SQ Sequence 202 AA;

Query Match 9.4%; Score 19; DB 8; Length 202;  
Best Local Similarity 100.0%; Pred. No. 2.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVARRRPWGKFAAETIRDPKK 120  
DB 79 GVARRRPWGKFAAETIRDPKK 97

RESULT 5  
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ID ADM72375 standard; protein; 202 AA.  
AC ADM72375;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Soybean NRTF1d polypeptide.  
XX  
KW Plant; nematode-regulated polypeptide; calcium dependent protein kinase;  
KW CDPK; nematode-responsive transcription factor 1; NRTF1;  
KW nematode-responsive protein; NRP; caffeic acid 7-O-methyltransferase;  
KW 7OM; inositol 5-phosphatase; IPP; nematocidal; gene therapy;  
KW nematode resistance; soybean; enzyme; NRTF1d.  
XX  
OS Glycine max.  
XX  
PN WO2004029222-A2.  
XX  
PD 08-APR-2004.  
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PF 30-SEP-2003; 2003WO-US031029.  
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PR 30-SEP-2002; 2002US-0414771P.  
XX  
PS (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Hu X, Lu G;  
XX  
DR WPI; 2004-316104/29.  
XX  
DR N-PSDB; ADM72374.  
XX  
PD New isolated nucleic acid molecules encoding nematode-responsive  
PT proteins, useful for conferring or improving nematode resistance in  
PT plants.  
XX  
PS Claim 26; SEQ ID NO 13; 143pp; English.  
XX  
CC The invention relates to pathogen-responsive genes that encode a nematode  
CC -regulated polypeptides. The proteins of the invention include calcium  
CC dependent protein kinase (CDPK), nematode-responsive transcription factor  
CC 1 (NRTF1), nematode-responsive protein (NRP), caffeic acid 7-O-  
CC methyltransferase (7OM) or inositol 5-phosphatase (IPP) polypeptides. The  
CC nucleic acid molecule encoding the polypeptides are operably linked to a  
CC promoter that drives expression in a host cell. The composition and  
CC methods are useful for conferring or improving nematode resistance in  
CC plants. The present sequence represents a soybean NRTF1d polypeptide.  
XX  
SQ Sequence 202 AA;

Query Match 9.4%; Score 19; DB 8; Length 202;  
Best Local Similarity 100.0%; Pred. No. 2.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVARRRPWGKFAAETIRDPKK 120  
DB 79 GVARRRPWGKFAAETIRDPKK 97

RESULT 6  
AAG24800  
ID AAG24800 standard; protein; 212 AA.

XX AAG24800;  
AC  
XX 17-OCT-2000 (first entry)  
DT  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 28612.  
DE  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridization assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS  
XX EP1033405-A2.  
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XX 06-SEP-2000.  
PD  
XX 25-FEB-2000, 2000EP-00301439.  
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Query Match          9.4%; Score 19; DB 3; Length 212;
Best Local Similarity 100.0%; Pred.No. 2.8e-09;
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XX AAG34781 standard; protein; 212 AA.
AC AAG34781;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 42376.
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KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
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ID AAG34780 standard; protein; 226 AA.

AC AAG34780;  
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DT 18-OCT-2000 (first entry)  
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 42375.  
XX

KW Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.

OS Arabidopsis thaliana.  
XX

PN EP1033405-A2.

XX 06-SEP-2000.  
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XX AAG24799;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 28611.

KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

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PR 02-AUG-1999; 99US-0146388P.  
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PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-015138P.  
PR 01-SEP-1999; 99US-015130P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 22-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.

PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159337P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161933P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 9.4%; Score 19; DB 3; Length 226;  
Best Local Similarity 100.0%; Pred. No. 3e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAIRDPKK 120  
DB 94 GVRRRPWGKFAAIRDPKK 112

## RESULT 10

ID AAE02464 standard; protein; 226 AA.

XX AC AAE02464;

XX DT 10-AUG-2001 (first entry)

DE Arabidopsis thaliana transcription factor G22.

XX KM Transcription factor; environmental stress tolerance; gene therapy;

KM plant structure; plant development.

XX OS Arabidopsis thaliana.

XX FH Key Location/Qualifiers

FT Domain 89..157 /note="Conserved domain"

XX PN WO200136598-A1.

XX PD 25-MAY-2001.

PF 14-NOV-2000; 2000MO-US031458.

PR 17-NOV-1999; 99US-0166228P.

PR 17-APR-2000; 2000US-0197899P.

PR 22-AUG-2000; 2000US-0227439P.  
XX (MEND-) MENDEL BIOTECHNOLOGY INC.  
PA (PINE/) PINEDA O.

PA (YUGG/) YU G.  
 PA (CREE/) CREELMAN R.  
 PA (RIEC/) RIECHMANN J. L.  
 PA (HEAR/) HEARD J.  
 PA (RATC/) RATCLIFFE O.  
 PA (REUB/) REUBER L.  
 PA (KEDD/) KEDDIE J.  
 XX  
 PI Pineda O, Yu G, Creelman R, Riechmann JL, Heard J, Ratcliffe O,  
 PI Reuber L, Keddie J;  
 XX  
 DR WPI: 2001-336000/35.  
 DR N-PSDB; AAD06444.  
 XX  
 PT Nucleic acids encoding plant transcription factor polypeptides, useful  
 PT for altering the environmental stress tolerance characteristics of  
 PT plants.  
 XX  
 PS Claim 4; Page 55-56; 116pp; English.  
 XX  
 CC The present amino acid sequence is Arabidopsis thaliana transcription  
 CC factor. This novel transcription factor is useful for modifying a plant's  
 CC phenotype in desirable ways, such as modifying a plants environmental  
 CC stresses. The transcription factor is encoded by environmental stress  
 CC tolerance gene derived from Arabidopsis thaliana. The transcription  
 CC factors and the genes encoding them are used to alter the structure and  
 CC developmental characteristics of plants such as soybean, wheat, corn,  
 CC potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf,  
 CC banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot,  
 CC cauliflower, coffee, onion, cucumber, eggplant, grapes, honey dew,  
 CC lettuce, mango, melon, papaya, peas, pepper, pineapple, spinach, squash,  
 CC sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or  
 CC vegetable brassicas. These sequences are also used for modifying traits  
 CC associated with environmental stress tolerance, such as freezing,  
 CC chilling, heat, drought, water saturation, salt, photoconditions,  
 CC radiation and ozone. The transcription factors are used in gene therapy  
 CC  
 SQ Sequence 226 AA;  
 Query Match 9.4%; Score 19; DB 4; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 3e-09;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 102 GVRRRPWGKFAAEIRDPKK 120  
 Db 94 GVRRRPWGKFAAEIRDPKK 112  
 RESULT 11  
 ADE37189  
 ID ADE37189 standard; protein; 226 AA.  
 XX  
 AC ADE37189;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Plant yield related protein from clone G22.  
 XX  
 KW transcription factor; tolerance; environmental condition;  
 KW microbial disease; fungal disease; viral disease; pest infestation;  
 KW herbicide sensitivity; heavy metal tolerance; heavy metal uptake;  
 KW growth improvement; photocondition; nutrient uptake; hormone sensitivity;  
 KW transgenic plant.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WO2003014327-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 09-AUG-2002; 2002WO-US026966.  
 XX  
 PR 09-AUG-2001; 2001US-0310847P.

PR 19-NOV-2001; 2001US-0336049P.  
 PR 11-DEC-2001; 2001US-0338652P.  
 PR 14-JUN-2002; 2002US-00171468.  
 XX  
 PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LJ, Dubell AN;  
 PI Ratcliffe O, Pineda O, Yu GL, Brown PE;  
 XX  
 DR WPI: 2003-256576/25.  
 DR N-PSDB; ADE37188.  
 XX  
 PT New stress-related transcription factor polynucleotides and polypeptides,  
 PT useful for producing transgenic plants with e.g. improved tolerance to  
 PT diseases or pests, decreased herbicide sensitivity, or improved nutrient  
 PT uptake.  
 XX  
 PS Disclosure, SEQ ID NO 128; 470pp; English.  
 XX  
 CC The invention relates to a number of cDNA sequence and their encoded  
 CC proteins which are especially transcription factor cDNAs and their  
 CC proteins. The isolated or recombinant polynucleotide is useful for  
 CC producing a modified plant with a modified trait, e.g. enhanced tolerance  
 CC to environmental conditions, improved tolerance to microbial, fungal or  
 CC viral diseases, improved tolerance to pest infestation, decreased  
 CC herbicide sensitivity, improved tolerance of heavy metals, or enhanced  
 CC ability to take up heavy metals, improved growth under poor  
 CC photoconditions, improved nutrient uptake, or reduced hormone  
 CC sensitivity. The transgenic plants are useful for growing a progeny plant  
 CC comprising the desired trait. The polynucleotides and polypeptides are  
 CC also useful in bioinformatic search methods. This sequence represents one  
 CC of the proteins of the invention.  
 XX  
 SQ Sequence 226 AA;  
 Query Match 9.4%; Score 19; DB 7; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 3e-09;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 102 GVRRRPWGKFAAEIRDPKK 120  
 Db 94 GVRRRPWGKFAAEIRDPKK 112  
 RESULT 12  
 ADI41543  
 ID ADI41543 standard; protein; 226 AA.  
 XX  
 AC ADI41543;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Plant transcription factor #3.  
 XX  
 KW transgenic; plant; enhanced tolerance to abiotic stress;  
 KW glycosphate tolerance; hormone sensitivity; disease resistance;  
 KW sugar sensing; flowering; flower structure; stem bifurcation;  
 KW branching pattern; apical dominance; trichome; stem morphology;  
 KW root growth; root hair; seed development; cell proliferation;  
 KW cell differentiation; premature senescence; necrosis; plant size;  
 KW leaf morphology; seed morphology; seed biochemistry; root anhydrocytin;  
 KW plant anhydrocytin; light response; shade avoidance; bioinformatic;  
 KW transcription factor.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN US2004015927-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 25-FEB-2003; 2003US-00374780.  
 XX  
 PR 18-APR-2001; 2001US-00837944.

XX (SHER/) SHERMAN B K.  
 PA (RIEC/) RIECHMANN J L.  
 PA (JIANG/) JIANG C.  
 PA (HEAR/) HEARD J E.  
 PA (HAAR/) HAARE V.  
 PA (CREE/) CREELMAN R A.  
 PA (RATC/) RATCLIFFE O.  
 PA (ADAM/) ADAM L J.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J.  
 PA (BROU/) BROUN P E.  
 PA (PILG/) PILGRIM M L.  
 PA (DUBE/) DUBELL A N.  
 PA (PINE/) PINEDA O.  
 PA (YUGG/) YU G.  
 PI Sherman BK, Riechmann JI, Jiang C, Heard JE, Haake V,  
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE,  
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G,  
 XX WPI, 2004-132245/13.  
 DR N-PSDB; AD141542.  
 PT New transgenic plant comprising a recombinant polynucleotide of any one  
 PT of more than 500 nucleotide sequences, useful in bioinformatic search  
 PT methods.  
 XX Claim 1; SEQ ID NO 6; 435bp; English.  
 XX The invention describes a transgenic plant comprising a recombinant  
 CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 CC defined in the specification or its complement. The method of the  
 CC invention can be used to produce a plant having altered traits such as:  
 CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone  
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
 CC altered flower structure; change in stem bifurcations, altered branching  
 CC pattern, reduced apical dominance, reduced trichome density; lack of  
 CC trichomes; reduced ectopic trichome development; altered trichome  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; seed morphology; seed  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanins, or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This is the amino acid sequence of a plant  
 CC transcription factor that can be used in the creation of a transgenic  
 CC plant with altered traits.  
 XX  
 XX Sequence 226 AA;  
 SQ  
 Query Match 9.4%; Score 19; DB 8; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 3e-09; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0;  
 QY 102 GVARRRPWGKFAAEIRDPK 120  
 Db 94 GVARRRPWGKFAAEIRDPK 112  
 RESULT 13  
 ADO01615  
 ID ADO01615 standard; protein; 226 AA.  
 XX  
 AC ADO01615;  
 XX  
 DT 01-UTR-2004 (first entry)  
 XX  
 XX Thalecress transcription factor protein #14.  
 DE Thalecress transcription factor; plant; transgenic; abiotic stress;  
 XX  
 KM cold tolerance; heat tolerance; drought; osmotic stress;  
 KM phosphate limitation; potassium limitation; nitrogen limitation;  
 KM hormone sensitivity; disease resistance; sugar sensing; seed germination;  
 KM flowering; inflorescence architectural change;  
 KM meristem cell differentiation; phylloclaxy; apical dominance;  
 KM trichome development; seed development; premature senescence;  
 KM delayed senescence; lethality; necrosis; plant size; leaf morphology;  
 KM seed morphology; secondary metabolism; light response; shade avoidance.  
 XX Arabidopsis thaliana.  
 OS  
 XX  
 PN US2004045049-A1.  
 XX  
 XX 04-MAR-2004.  
 PD  
 XX  
 XX 10-APR-2003; 2003US-00412699.  
 XX  
 XX 13-SEP-1999; 99US-00394519.  
 PR 21-JAN-2000; 2000US-00489376.  
 PR 17-FEB-2000; 2000US-00506720.  
 PR 22-MAR-2000; 2000US-00532591.  
 PR 22-MAR-2000; 2000US-00533029.  
 PR 22-MAR-2000; 2000US-00533030.  
 PR 22-MAR-2000; 2000US-00533392.  
 PR 22-MAR-2000; 2000US-00533648.  
 PR 06-APR-2000; 2000MO-US009448.  
 PR 16-NOV-2000; 2000US-00713994.  
 PR 27-MAR-2001; 2001US-00819142.  
 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JAN-2002; 2002US-00958131.  
 PR 14-JUN-2002; 2002US-00171468.  
 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
 PR 09-AUG-2002; 2002US-00225068.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 25-FEB-2003; 2003US-00374780.  
 XX  
 XX (ZHAN/) ZHANG J.  
 PA (FROM/) FROMM M E.  
 PA (HEAR/) HEARD J E.  
 PA (RIEC/) RIECHMANN J L.  
 PA (ADAM/) ADAM L J.  
 PA (BROU/) BROUN P E.  
 PA (PINE/) PINEDA O.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J S.  
 PA (YUGG/) YU G.  
 PA (JIANG/) JIANG C.  
 PA (SAMA/) SAMAHA R S.  
 PA (PILG/) PILGRIM M L.  
 PA (CREE/) CREELMAN R A.  
 PA (DUBE/) DUBELL A N.  
 PA (RATC/) RATCLIFFE O.  
 PA (KIMI/) KIMIMOTO R.  
 PA (SHER/) SHERMAN B K.  
 PI Zhang J, Fromm ME, Heard JE, Riechmann JI, Adam LJ, Brown PE,  
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS,  
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kimimoto R,  
 PI Sherman BK;  
 XX  
 DR WPI, 2004-225755/21.  
 DR N-PSDB; ADO01614.  
 XX  
 PT New transgenic plant, useful in developing phenotypes with altered or  
 PT improved characteristics or traits.  
 XX  
 PS Claim 1; SEQ ID NO 28; 213bp; English.  
 XX  
 CC The invention relates to a transgenic plant comprising a recombinant  
 CC polynucleotide having a polynucleotide sequence or its complementary  
 CC sequence comprising a sequence encoding a polypeptide, that initiates  
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,

Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588 -AD003527 or ADO03530-AD003559. Also included are using a transgenic plant to grow a progeny plant, an expression cassette (comprising a constitutive, inducible or tissue-specific promoter and a recombinant polynucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polynucleotide sequence and identifying at least one downstream polynucleotide sequence that is subject to a regulatory effect of any of the polypeptides encoded by the polynucleotide described above. The transgenic plant is useful for producing a plant that has an altered trait e.g. an enhanced tolerance to abiotic stress (increased tolerance to chilling, germination in cold conditions, freezing tolerance, tolerance to heat, tolerance to drought, tolerance to osmotic stress, tolerance to salt, tolerance to phosphate limitation, tolerance to potassium limitation, decreased sensitivity to nitrogen limitation), altered hormone sensitivity, reduced sensitivity to abscisic acid, an altered response to ethylene, disease resistance, altered susceptibility to Botrytis, altered susceptibility to Fusarium, altered susceptibility to Erwinia, altered susceptibility to Pseudomonas syringae, altered susceptibility to Sclerotinia, altered sugar sensing, improved seed germination and seedling vigor, early flowering, late flowering, extended period of flowering, an inflorescence architectural change, a change in stem bifurcations, a lack of a shoot meristem, reduced meristem cell differentiation, altered phyllotaxy, altered branching pattern, reduced apical dominance, reduced trichome density, ectopic trichome development, altered trichome development, altered stem morphology, increased root growth, increased root hairs, altered seed development, altered cell proliferation/cell differentiation, premature senescence, delayed senescence, lethality, increased necrosis, an increase in seedling or plant size, decreased plant size, a change in leaf morphology, increased altered leaf development, increased leaf size and mass, glossy leaves, leaf cell expansion, change in seed morphology, altered seed coloration, increased seed size, decreased seed size, altered seed shape, change in leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid content, increased leaf insoluble sugars, decreased leaf insoluble sugars, increased leaf anthocyanins, an alteration of leaf fatty acid content, an alteration of leaf glucosinolate content, change in seed biochemistry, an increase in seed oil content, decrease in seed oil content, increase in seed fatty acid content, decrease in seed fatty acid content, increase in seed protein content, decrease in seed protein content, alteration in seed prenyl lipid content, increase in seed sterols, upregulation of genes involved in secondary metabolism, increase in root anthocyanins, increase in plant anthocyanins, and alteration in light response or shade avoidance. The present sequence represents a chalcress transcription factor of the invention.

SO Sequence 226 AA;

Query Match 9.4%; Score 19; DB 8; Length 226;  
Best Local Similarity 100.0%; Pred. No. 3e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAIEIRDPKK 120  
DB 94 GVRRRPWGKFAAIEIRDPKK 112

RESULT 14

ADN73807 standard; protein; 226 AA.

ADN73807;

15-JUL-2004 (first entry)

Thale cress protein repressed in E2Fa/Dpa expressing plants SegID 1702.

plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;

animal feed product; thale cress; cell wall biosynthesis;

nitrogen metabolism; carbon metabolism.

Arabidopsis thaliana.

XX MO2004035796-A2.  
XX 29-APR-2004.  
XX 20-OCT-2003; 2003MO-EP011658.  
XX 18-OCT-2002; 2002EP-00079408.  
XX (CROP-) CROPDESIGN NV.  
XX Inze D, De Veylder L, Vlieghe K;  
XX WPI; 2004-348466/32.  
XX N-PSDB; ADN73806.  
XX Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or more proteins.

Claim 1; SEQ ID NO 1702; 134bp; English.

This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up- or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilization and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene repressed 1.3 fold or more in plants overexpressing the E2Fa/Dpa transcription factor, given in an exemplification of the invention.

SO Sequence 226 AA;

Query Match 9.4%; Score 19; DB 8; Length 226;  
Best Local Similarity 100.0%; Pred. No. 3e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAIEIRDPKK 120  
DB 94 GVRRRPWGKFAAIEIRDPKK 112

RESULT 15

AAV97227 standard; protein; 210 AA.

AAV97227;

19-DEC-2000 (first entry)

Plant transcription factor AP2 DNA-binding domain polypeptide.

AP2; transcription factor; plant metabolism; metabolite; primary;

secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;

food colouring; flavouring; fragrance; antimicrobial; pathogenic;

insecticide; gene expression; modulation.

Catharanthus roseus.

MO200046383-A2.



XX 10-AUG-2000.  
 PD  
 XX  
 PF 07-FEB-2000; 2000MO-NL000075.  
 XX  
 PR 05-FEB-1999; 99DK-00000158.  
 PR 10-FEB-1999; 99US-0119388P.  
 XX  
 PA (UYLE-) RIJCKUNIV LEIDEN.  
 XX  
 PI Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW,  
 XX  
 DR WPI; 2000-499380/44.  
 XX N-PSDB; AAA53744.  
 XX  
 PT Modulating level of metabolites and stress resistance in recombinant  
 PT cells for synthesis of plant metabolites such as alkaloids including  
 PT terpenoid indole alkaloids, by providing transcription factor to the  
 PT cell.  
 XX  
 PS Disclosure; Page 97; 101pp; English.  
 XX  
 CC Many plant secondary metabolites have value as pharmaceuticals, food  
 CC colourings, flavours and fragrances. Some plant secondary metabolites are  
 CC linked to plant or plant cell defence mechanisms and may confer to the  
 CC plant antimicrobial activity, protection against UV light, herbivores,  
 CC pathogens, insects and nematodes. Plant secondary metabolites such as  
 CC terpenoid indole alkaloids (TIA) represent a class of pharmaceutically  
 CC useful compounds which naturally occur in many plant species. New methods  
 CC are described which modulate the expression of one or more genes involved  
 CC in the biosynthesis of plant metabolites or their precursors in plant  
 CC cells. The method comprises inserting into a plant cell a sequence  
 CC encoding a transcription factor comprising an AP2 DNA-binding domain and  
 CC by modifying the expression of that transcription factor. Transcription  
 CC factors comprising an AP2 DNA-binding domain are useful as central  
 CC regulators of complex metabolite pathways involving numerous target genes  
 CC for such transcription factors. This means that the yield of commercially  
 CC valuable metabolite compounds can be enhanced and the tolerance of plants  
 CC towards exogenous stress factors can be influenced. The method is useful  
 CC for modulating the level of one or more metabolites. By providing a  
 CC transcription factor to the cell the level of the metabolite is enhanced  
 CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to  
 CC a cell to which the transcription factor is not provided  
 XX  
 SQ Sequence 210 AA;

Query Match 8.3%; Score 18; DB 3; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAEIRDPK 119  
 |||||  
 Db 129 GVRRRPWGKFAEIRDPK 146

Search completed: February 27, 2005, 22:23:23  
 Job time : 166 secs

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OM protein - protein search, using sw model

Run on: February 27, 2005, 22:18:21 ; Search time 43 Seconds  
(without alignments)  
352.413 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 203  
Sequence: 1 MSERISVSDRFLSLIEH.....SSSSSSSSSSSGRRKRRY 203

Scoring table: OLIGO  
Gapop 60.0 , Gapept 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/prodata/1/1aa/5B COMB.pep:.\*  
3: /cgn2\_6/prodata/1/1aa/6A COMB.pep:.\*  
4: /cgn2\_6/prodata/1/1aa/6B COMB.pep:.\*  
5: /cgn2\_6/prodata/1/1aa/PC/US COMB.pep:.\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	17	8.4	60	US-09-300-672-9	Sequence 9, Appl
2	17	8.4	69	US-08-912-272-17	Sequence 17, Appl
3	17	8.4	69	US-09-026-039-17	Sequence 17, Appl
4	13	6.4	59	US-09-202-161B-25	Sequence 25, Appl
5	13	6.4	61	US-08-949-603-11	Sequence 11, Appl
6	13	6.4	61	US-08-706-270A-11	Sequence 11, Appl
7	13	6.4	61	US-08-949-580-11	Sequence 11, Appl
8	13	6.4	61	US-08-950-172A-11	Sequence 11, Appl
9	13	6.4	61	US-09-198-119C-11	Sequence 11, Appl
10	13	6.4	61	US-09-601-802D-11	Sequence 11, Appl
11	13	6.4	63	US-09-601-802D-134	Sequence 134, Appl
12	13	6.4	69	US-08-912-272-18	Sequence 18, Appl
13	13	6.4	69	US-08-912-272-20	Sequence 20, Appl
14	13	6.4	69	US-09-026-039-18	Sequence 18, Appl
15	13	6.4	69	US-09-026-039-20	Sequence 20, Appl
16	13	6.4	231	US-09-202-161B-1	Sequence 1, Appl
17	13	6.4	243	US-09-533-029-34	Sequence 34, Appl
18	13	6.4	268	US-09-533-029-18	Sequence 18, Appl
19	12	5.9	462	US-09-248-796A-14808	Sequence 14808, A
20	12	5.4	101	US-09-640-211A-921	Sequence 921, App
21	11	5.4	505	US-09-248-796A-14299	Sequence 14299, A
22	10	4.9	130	US-08-630-822A-90	Sequence 90, Appl
23	10	4.9	130	US-09-005-069-90	Sequence 90, Appl
24	10	4.9	130	US-09-171-156A-39	Sequence 39, Appl
25	10	4.9	130	US-09-004-730A-39	Sequence 39, Appl
26	10	4.9	130	US-08-981-799A-39	Sequence 39, Appl
27	10	4.9	141	US-09-828-303-17	Sequence 17, Appl

28	10	4.9	153	4	US-09-248-796A-28015	Sequence 28015, A
29	10	4.9	175	4	US-09-248-796A-23457	Sequence 23457, A
30	10	4.9	203	4	US-09-270-767-35326	Sequence 35326, A
31	10	4.9	203	4	US-09-270-767-50543	Sequence 50543, A
32	10	4.9	246	3	US-09-185-160-7	Sequence 7, Appl
33	10	4.9	249	4	US-09-248-796A-27128	Sequence 27128, A
34	10	4.9	256	4	US-09-485-529-5	Sequence 5, Appl
35	10	4.9	258	4	US-09-485-529-20	Sequence 20, Appl
36	10	4.9	266	4	US-09-248-796A-14280	Sequence 14280, A
37	10	4.9	273	4	US-09-248-796A-25975	Sequence 25975, A
38	10	4.9	289	4	US-09-270-767-60136	Sequence 60136, A
39	10	4.9	291	4	US-09-248-796A-14273	Sequence 14273, A
40	10	4.9	349	3	US-09-162-524-3	Sequence 3, Appl
41	10	4.9	367	3	US-08-213-419B-15	Sequence 15, Appl
42	10	4.9	379	4	US-09-270-767-34013	Sequence 34013, A
43	10	4.9	379	4	US-09-270-767-49230	Sequence 49230, A
44	10	4.9	382	3	US-08-213-419B-19	Sequence 19, Appl
45	10	4.9	408	4	US-09-802-213-9	Sequence 9, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-300-672-9
; Sequence 9, Application US/09300672
; Patent No. 6248937
; GENERAL INFORMATION:
; APPLICANT: Finkelstein, Ruth R.
; APPLICANT: Lynch, Tim
; APPLICANT: Goodman, Howard M.
; APPLICANT: Wang, Ming-li
; TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
; FILE REFERENCE: 480.89 (HV)
; CURRENT APPLICATION NUMBER: US/09/300,672
; CURRENT FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Ap2 domain protein
US-09-300-672-9

Query Match      8.4%; Score 17; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 9e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAIRIDP 118
Db      3 GVRRRPWGKFAIRIDP 19

RESULT 2
US-08-912-272-17
; Sequence 17, Application US/08912272
; Patent No. 6093874
; GENERAL INFORMATION:
; APPLICANT: Jofuku, K. Diane
; APPLICANT: Okamoto, Jack K.
; TITLE OF INVENTION: Methods for Improving Seeds
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; City: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,272
FILING DATE: 15-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,152
FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baetlian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..69
OTHER INFORMATION: /note="AP2 domain within tobacco"
FEATURE:
NAME/KEY: Region
LOCATION: 36..51
OTHER INFORMATION: /note="putative EREBP-1 amphipathic
OTHER INFORMATION: alpha-helix"
US-08-912-272-17
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Query Match      8.4%; Score 17; DB 3; Length 69;
Best local Similarity 100.0%; Pred. No. 1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      102 GVRRRPWGKFAAEIRDP 118
      |||
Db      6 GVRRRPWGKFAAEIRDP 22
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RESULT 3
US-09-026-039-17
Sequence 17, Application US/09026039
Patent No. 6329567
GENERAL INFORMATION:
APPLICANT: Jofuku, K. Diane
APPLICANT: Okamoto, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,039
FILING DATE: 19-FEB-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/912,272
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,152
FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baetlian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067230US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..69
OTHER INFORMATION: /note="AP2 domain within tobacco"
FEATURE:
NAME/KEY: Region
LOCATION: 36..51
OTHER INFORMATION: /note="putative EREBP-1 amphipathic
OTHER INFORMATION: alpha-helix"
US-09-026-039-17
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```
Query Match      8.4%; Score 17; DB 3; Length 69;
Best local Similarity 100.0%; Pred. No. 1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      102 GVRRRPWGKFAAEIRDP 118
      |||
Db      6 GVRRRPWGKFAAEIRDP 22
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RESULT 4
US-09-202-161B-25
Sequence 25, Application US/09202161B
Patent No. 665353
GENERAL INFORMATION:
APPLICANT: Purdue Research Foundation
TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
FILE REFERENCE: 7024-371
CURRENT APPLICATION NUMBER: US/09/202,161B
PRIOR FILING DATE: 1997-06-12
PRIOR APPLICATION NUMBER: PCT/US97/10382
PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION NUMBER: 60/019,633
PRIOR FILING DATE: 1996-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: ASCII
SEQ ID NO 25
LENGTH: 59
TYPE: PRT
ORGANISM: Lycopersicon esculentum
US-09-202-161B-25
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Query Match      6.4%; Score 13; DB 4; Length 59;
Best local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      106 RPWGKFAAEIRDP 118
      |||
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Db 8 RFWGKFAAIRDP 20

## RESULT 5

US-08-949-603-11  
; Sequence 11, Application US/08949603  
; Patent No. 5891859  
; GENERAL INFORMATION:  
; APPLICANT: Michael F. Thomashow and  
; TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
; TITLE OF INVENTION: WHICH REGULATES COLD AND  
; TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS 5.00  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/949,603  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/706,270  
; FILING DATE: September 4, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20,931  
; REFERENCE/DOCKET NUMBER: MSU 4.1-384  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: No. 5891859e  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Polypeptide  
; HYPOTHETICAL: No  
; ANTI-SENSE: No  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM: Tobacco  
; STRAIN:  
; INDIVIDUAL ISOLATE: N/A  
; DEVELOPMENTAL STAGE: N/A  
; HAPLOTYPE: N/A  
; TISSUE TYPE: N/A  
; CELL TYPE: N/A  
; CELL LINE: N/A  
; ORGANELLE: N/A  
; IMMEDIATE SOURCE: N/A  
; POSITION IN GENOME: N/A  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD: sequencing  
; OTHER INFORMATION: Figure 2D  
; PUBLICATION INFORMATION:  
; US-08-949-603-11

Query Match 6.4%; Score 13; DB 2; Length 61;

Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 RFWGKFAAIRDP 118

Db 8 RFWGKFAAIRDP 20

## RESULT 6

US-08-706-270A-11  
; Sequence 11, Application US/08706270A  
; Patent No. 5892009  
; GENERAL INFORMATION:  
; APPLICANT: Michael F. Thomashow and  
; TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
; TITLE OF INVENTION: WHICH REGULATES COLD AND  
; TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS 5.00  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/706,270A  
; FILING DATE: September 4, 1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20,931  
; REFERENCE/DOCKET NUMBER: MSU 4.1-310  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: No. 5892009e  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Polypeptide  
; HYPOTHETICAL: No  
; ANTI-SENSE: No  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM: Tobacco  
; STRAIN:  
; INDIVIDUAL ISOLATE: N/A  
; DEVELOPMENTAL STAGE: N/A  
; HAPLOTYPE: N/A  
; TISSUE TYPE: N/A  
; CELL TYPE: N/A  
; CELL LINE: N/A  
; ORGANELLE: N/A  
; IMMEDIATE SOURCE: N/A  
; POSITION IN GENOME: N/A  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD: sequencing

OTHER INFORMATION: Figure 2D  
PUBLICATION INFORMATION:  
US-08-706-270A-11

Query Match 6.4%; Score 13; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 RFWGKFAAEIRDP 118  
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Db 8 RFWGKFAAEIRDP 20

RESULT 7  
US-08-949-580-11  
Sequence 11, Application US/08949580  
Patent No. 5929305  
GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and  
APPLICANT: Eric J. Stockinger  
TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,580  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/706,270  
FILING DATE: September 4, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5929305e  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61  
TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Tobacco  
STRAIN:  
INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: N/A

POSITION IN GENOME: N/A  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: sequencing  
PUBLICATION INFORMATION:  
US-08-949-580-11

Query Match 6.4%; Score 13; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 RFWGKFAAEIRDP 118  
|||||  
Db 8 RFWGKFAAEIRDP 20

RESULT 8  
US-08-950-172A-11  
Sequence 11, Application US/08950172A  
Patent No. 5965705  
GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and  
APPLICANT: Eric J. Stockinger  
TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/950,172A  
FILING DATE: 10/14/1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/949,580  
FILING DATE: October 14, 1997  
APPLICATION NUMBER: 08/706,270  
FILING DATE: September 4, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5965705e  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61  
TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Tobacco  
STRAIN:  
INDIVIDUAL ISOLATE: N/A

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DEVELOPMENTAL STAGE: N/A
HAPOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE: N/A
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD: sequencing
OTHER INFORMATION: Figure 2D
PUBLICATION INFORMATION:
US-08-950-172A-11

Query Match      6.4%; Score 13; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      106 RPKGKFAAIRDP 118
Db      8 RPKGKFAAIRDP 20

RESULT 9
US-09-198-119C-11
; Sequence 11, Application US/09198119C
; Patent No. 6417428
; GENERAL INFORMATION:
; APPLICANT: Thomashow, Michael
; APPLICANT: Stockinger, Eric
; APPLICANT: Jaglo-Ottosen, Kirsten
; APPLICANT: Gilmour, Sarah
; APPLICANT: Zarka, Daniel
; APPLICANT: Jiang, Cai-Zhong
; TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance
; FILE REFERENCE: 19117, 713 Seq List
; CURRENT APPLICATION NUMBER: US/09/198,119C
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 08/706,270
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/018,233
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/017,816
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,235
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/017,575
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,227
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,234
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-198-119C-11

Query Match      6.4%; Score 13; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      106 RPKGKFAAIRDP 118
Db      8 RPKGKFAAIRDP 20

RESULT 10
US-09-601-802D-11
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; Sequence 11, Application US/09601802D
; Patent No. 6706866
; GENERAL INFORMATION:
; APPLICANT: Thomashow, Michael
; APPLICANT: Stockinger, Eric
; APPLICANT: Jaglo-Ottosen, Kirsten
; APPLICANT: Gilmour, Sarah
; APPLICANT: Zarka, Daniel
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Zhang, James
; APPLICANT: Haake, Volker
; TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
; FILE REFERENCE: 51442000201/MB10029
; CURRENT APPLICATION NUMBER: US/09/601,802D
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US/09/601,802D
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/018,233
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,816
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/018,235
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,575
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-601-802D-11

Query Match      6.4%; Score 13; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      106 RPKGKFAAIRDP 118
Db      8 RPKGKFAAIRDP 20

RESULT 11
US-09-601-802D-134
; Sequence 134, Application US/09601802D
; Patent No. 6706866
; GENERAL INFORMATION:
; APPLICANT: Thomashow, Michael
; APPLICANT: Stockinger, Eric
; APPLICANT: Jaglo-Ottosen, Kirsten
; APPLICANT: Gilmour, Sarah
; APPLICANT: Zarka, Daniel
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Zhang, James
; APPLICANT: Haake, Volker
; TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
; FILE REFERENCE: 51442000201/MB10029
; CURRENT APPLICATION NUMBER: US/09/601,802D
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/018,233
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,816
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/018,235
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,575
; PRIOR FILING DATE: 1998-02-03
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;; PRIOR APPLICATION NUMBER: 09/018,227  
;; PRIOR FILING DATE: 1998-02-03  
;; PRIOR APPLICATION NUMBER: 09/018,234  
;; PRIOR FILING DATE: 1998-02-03  
;; PRIOR APPLICATION NUMBER: 09/198,119  
;; PRIOR FILING DATE: 1998-11-23  
;; NUMBER OF SEQ ID NOS: 259  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
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;; LENGTH: 63  
;; TYPE: PRT  
;; ORGANISM: Nicotiana tabacum  
US-09-601-802D-134

Query Match 6.4%; Score 13; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAAEIRDP 118  
Db 10 RFWGKFAAEIRDP 22

RESULT 12  
US-08-912-272-18  
; Sequence 18, Application US/08912272  
; Patent No. 6093874  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamoto, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,272  
; FILING DATE: 15-AUG-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baebian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067220US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..69  
; OTHER INFORMATION: /note="Ap2 domain within tobacco  
; OTHER INFORMATION: EREBP-2"

;; FEATURE:  
;; NAME/KEY: Region  
;; LOCATION: 35..51  
;; OTHER INFORMATION: /note="putative EREBP-2 amphipathic  
;; OTHER INFORMATION: alpha-helix"  
US-08-912-272-18

Query Match 6.4%; Score 13; DB 3; Length 69;  
Best Local Similarity 100.0%; Pred. No. 6.8e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAAEIRDP 118  
Db 10 RFWGKFAAEIRDP 22

RESULT 13  
US-08-912-272-20  
; Sequence 20, Application US/08912272  
; Patent No. 6093874  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamoto, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,272  
; FILING DATE: 15-AUG-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baebian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067220US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..69  
; OTHER INFORMATION: /note="Ap2 domain within tobacco  
; OTHER INFORMATION: EREBP-4"  
; NAME/KEY: Region  
; LOCATION: 35..51  
; OTHER INFORMATION: /note="putative EREBP-4 amphipathic  
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US-08-912-272-20



Query Match 6.4%; Score 13; DB 3; Length 69;  
Best Local Similarity 100.0%; Pred. No. 6.8e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAEIRDP 118  
Db 10 RPKGKFAEIRDP 22

## RESULT 14

US-09-026-039-18  
; Sequence 18; Application US/09026039  
; Patent No. 6329567  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamuro, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,039  
; FILING DATE: 19-FEB-1998  
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; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,272  
; FILING DATE: 15-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067230US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
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; LOCATION: 1..69  
; OTHER INFORMATION: /note="AP2 domain within tobacco  
; OTHER INFORMATION: EREBP-2"  
; FEATURE:  
; NAME/KEY: Region  
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; OTHER INFORMATION: /note="putative EREBP-2 amphipathic  
; OTHER INFORMATION: alpha-helix"  
US-09-026-039-18

Query Match 6.4%; Score 13; DB 3; Length 69;  
Best Local Similarity 100.0%; Pred. No. 6.8e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAEIRDP 118  
Db 10 RPKGKFAEIRDP 22

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US-09-026-039-20  
; Sequence 20; Application US/09026039  
; Patent No. 6329567  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamuro, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
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; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,272  
; FILING DATE: 15-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067230US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..69  
; OTHER INFORMATION: /note="AP2 domain within tobacco  
; OTHER INFORMATION: EREBP-4"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 35..51  
; OTHER INFORMATION: /note="putative EREBP-4 amphipathic  
; OTHER INFORMATION: alpha-helix"  
US-09-026-039-20

Query Match 6.4%; Score 13; DB 3; Length 69;  
Best Local Similarity 100.0%; Pred. No. 6.8e-05;  
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QY 106 RPKGKFAEIRDP 118  
Db 10 RPKGKFAEIRDP 22

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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	11.3	137	US-10-425-114-52229	Sequence 52229, A
2	23	11.3	146	US-10-424-599-214399	Sequence 214399, A
3	23	11.3	199	US-10-424-599-214365	Sequence 214365, A
4	23	11.3	203	US-10-425-114-36689	Sequence 36689, A
5	19	9.4	156	US-10-424-599-208822	Sequence 208822, A
6	19	9.4	202	US-10-424-599-175489	Sequence 175489, A
7	19	9.4	226	US-10-425-068-128	Sequence 128, App
8	19	9.4	226	US-10-374-780A-6	Sequence 6, Appl
9	19	9.4	226	US-10-412-699B-28	Sequence 28, Appl
10	17	8.4	124	US-10-374-780A-1737	Sequence 1737, Ap
11	17	8.4	139	US-09-934-455-6	Sequence 6, Appl
12	17	8.4	139	US-10-225-068-46	Sequence 46, Appl
13	17	8.4	139	US-10-225-066A-170	Sequence 170, App

14	17	8.4	139	US-10-374-780A-332	Sequence 332, App
15	17	8.4	152	US-10-425-114-41831	Sequence 41831, A
16	17	8.4	178	US-10-424-599-174805	Sequence 174805, A
17	17	8.4	201	US-10-225-066A-788	Sequence 788, App
18	17	8.4	201	US-10-374-780A-2230	Sequence 2230, App
19	17	8.4	201	US-10-412-699B-50	Sequence 50, Appl
20	17	8.4	201	US-10-412-699B-1726	Sequence 1726, Ap
21	17	8.4	207	US-10-278-536-54	Sequence 54, Appl
22	17	8.4	207	US-10-412-699B-54	Sequence 54, Appl
23	17	8.4	209	US-10-424-599-173483	Sequence 173483, A
24	17	8.4	214	US-10-425-114-37800	Sequence 37800, A
25	17	8.4	222	US-10-425-114-39220	Sequence 39220, A
26	17	8.4	224	US-10-425-114-41699	Sequence 41699, A
27	17	8.4	282	US-10-374-780A-503	Sequence 503, App
28	17	8.4	299	US-10-374-780A-1157	Sequence 1157, App
29	17	8.4	299	US-10-412-699B-1360	Sequence 1360, App
30	17	8.4	299	US-10-437-963-156010	Sequence 156010, A
31	17	8.4	1040	US-10-437-963-120630	Sequence 120630, A
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33	16	7.9	131	US-10-062-254-220	Sequence 220, App
34	16	7.9	131	US-10-374-780A-1736	Sequence 1736, App
35	16	7.9	150	US-10-424-599-223956	Sequence 223956, A
36	16	7.9	157	US-10-424-599-149169	Sequence 149169, A
37	16	7.9	218	US-09-934-455-192	Sequence 192, App
38	16	7.9	218	US-10-225-068-210	Sequence 210, App
39	16	7.9	218	US-10-225-066A-58	Sequence 58, Appl
40	16	7.9	218	US-10-225-067-70	Sequence 70, Appl
41	16	7.9	218	US-10-374-780A-252	Sequence 252, App
42	16	7.9	218	US-10-412-699B-800	Sequence 800, App
43	16	7.9	218	US-10-424-599-154832	Sequence 154832, A
44	16	7.9	220	US-10-425-114-40926	Sequence 40926, A
45	16	7.9	224	US-10-424-599-160662	Sequence 160662, A

## ALIGNMENTS

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; Sequence 52229, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 73128
; SEQ ID NO 52229
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700869231_FLI.pep
US-10-425-114-52229
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; Sequence 214399, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214399
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3562C.1.pep
US-10-424-599-214399

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Best Local Similarity 100.0%; Pred. No. 7.8e-13;
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; Sequence 214365, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214365
; LENGTH: 199
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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3559C.1.pep
US-10-424-599-214365

Query Match          11.3%; Score 23; DB 15; Length 199;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 36689, Application US/10425114
; Publication No. US20040031488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic David K
; APPLICANT: Screen, Steven B
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
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; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36689
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3093-015-B5_F1.1.pep
US-10-425-114-36689

Query Match          11.3%; Score 23; DB 15; Length 203;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 208822, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 208822
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; ORGANISM: Glycine max
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DB      69 GVRRRPWGKFAAEIRDPK 87

RESULT 6
US-10-424-599-175489
; Sequence 175489, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
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; TYPE: PRT
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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_129485C.1.pap
US-10-424-599-175489

Query Match
Best Local Similarity 9.4%; Score 19; DB 15; Length 202;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPMGKFAAETIRDPKK 120
DB 79 GVRRRPMGKFAAETIRDPKK 97

RESULT 7
US-10-225-068-128
; Sequence 128, Application US/10225068
; Publication No. US20030217383A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Adam, Luc J.
; APPLICANT: Dubell, Arnold T.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Brown, Pierre E.
; TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
; FILE REFERENCE: 514442002040
; CURRENT APPLICATION NUMBER: US/10/225,068
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (89)...(157)
; OTHER INFORMATION: Conserved domain
US-10-225-068-128

Query Match
Best Local Similarity 9.4%; Score 19; DB 15; Length 226;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPMGKFAAETIRDPKK 120
DB 94 GVRRRPMGKFAAETIRDPKK 112

RESULT 8
US-10-374-780A-6
; Sequence 6, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
```

```
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G22 (conserved domain in AA coordinates: 89-157)
US-10-374-780A-6

Query Match
Best Local Similarity 9.4%; Score 19; DB 15; Length 226;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPMGKFAAETIRDPKK 120
DB 94 GVRRRPMGKFAAETIRDPKK 112

RESULT 9
US-10-412-699B-28
; Sequence 28, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Brown, Pierre E.
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: Dubell, Arnold N.
```

```
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Kumimoto, Roderick
/ APPLICANT: Sherman, Bradley K.
/ TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
/ FILE REFERENCE: MBI-0048CIP
/ CURRENT APPLICATION NUMBER: US/10/412,699B
/ PRIOR FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: 09/394,519
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: 09/489,376
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: 09/506,720
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 09/533,030
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,392
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,029
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/532,591
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,648
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/713,994
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 09/819,142
/ PRIOR FILING DATE: 2001-03-27
/ REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2011
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 28
/ LENGTH: 226
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/ OTHER INFORMATION: G22
/ US-10-412-699B-28

Query Match          9.4%; Score 19; DB 15; Length 226;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      102 GVRRRPWGKFAAEIRDPK 120
      |||||
Db      94 GVRRRPWGKFAAEIRDPK 112
```

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RESULT 10
/ US-10-374-780A-1737
/ Sequence 1737, Application US/10374780A
/ Publication No. US20040019927A1
/ GENERAL INFORMATION:
/ APPLICANT: Sherman, Bradley K
/ APPLICANT: Riechmann, Jose Luis
/ APPLICANT: Jiang, Cai-Zhong
/ APPLICANT: Heard, Jacqueline E
/ APPLICANT: Haake, Volker
/ APPLICANT: Creelman, Robert A
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Adam, Luc J
/ APPLICANT: Reuber, T. Lynne
/ APPLICANT: Keddie, James E
/ APPLICANT: Brown, Pierre E
/ APPLICANT: Pilgrim, Marsha L
/ APPLICANT: Dubell III, Arnold T
/ APPLICANT: Pineda, Omaira
/ APPLICANT: Yu, Guo-Liang
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
/ FILE REFERENCE: MBI-0047 CIP
/ CURRENT APPLICATION NUMBER: US/10/374,780A
/ PRIOR FILING DATE: 2003-02-25
/ PRIOR APPLICATION NUMBER: 09/837,944
/ PRIOR FILING DATE: 2001-04-18
```

```
/ PRIOR APPLICATION NUMBER: 60/310,847
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: 09/934,455
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/336,049
/ PRIOR FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: 60/338,692
/ PRIOR FILING DATE: 2001-12-11
/ PRIOR APPLICATION NUMBER: 10/171,468
/ PRIOR FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 10/225,066
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 10/225,067
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 10/225,068
/ PRIOR FILING DATE: 2002-08-09
/ NUMBER OF SEQ ID NOS: 2906
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1737
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Oryza sativa japonica
/ FEATURE:
/ OTHER INFORMATION: G3383 Orthologous to G1792
/ US-10-374-780A-1737

Query Match          8.4%; Score 17; DB 15; Length 124;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      102 GVRRRPWGKFAAEIRDP 118
      |||||
Db      15 GVRRRPWGKFAAEIRDP 31
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```
RESULT 11
/ US-09-934-455-6
/ Sequence 6, Application US/09934455
/ Publication No. US20030121070A1
/ GENERAL INFORMATION:
/ APPLICANT: Adam, Luc
/ APPLICANT: Creelman, Robert
/ APPLICANT: Dubell, Arnold
/ APPLICANT: Heard, Jacqueline
/ APPLICANT: Jiang, Cai-Zhong
/ APPLICANT: Keddie, James
/ APPLICANT: Pilgrim, Marsha
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Reuber, Lynne
/ APPLICANT: Riechmann, Jose Luis
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Pineda, Omaira
/ TITLE OF INVENTION: Genes for Modifying Plant Traits IV
/ FILE REFERENCE: MBI-0025
/ CURRENT APPLICATION NUMBER: US/09/934,455
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227439
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: MBI-0022
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: MBI-0023
/ PRIOR FILING DATE: 2001-04-17
/ NUMBER OF SEQ ID NOS: 516
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 139
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/ US-09-934-455-6
```

```
Query Match          8.4%; Score 17; DB 10; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      102 GVRRRPWGKFAAEIRDP 118
      |||||
Db      22 GVRRRPWGKFAAEIRDP 38

RESULT 12
US-10-225-066A-46
; Sequence 46, Application US/10225068
; Publication No. US20030217383A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Adam, Luc J.
; APPLICANT: Dubell, Arnold T.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pineda, Omalra
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Broun, Pierre E.
; TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
; FILE REFERENCE: 514442002040
; CURRENT APPLICATION NUMBER: US/10/225,068
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17)...(85)
; OTHER INFORMATION: Conserved domain
US-10-225-066A-46

Query Match      8.4%; Score 17; DB 15; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAEIRDP 118
      |||||
Db      22 GVRRRPWGKFAAEIRDP 38

RESULT 13
US-10-225-066A-170
; Sequence 170, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Dubell, Arnold T.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Creelman, Robert A.
; APPLICANT: Pineda, Omalra
; APPLICANT: Yu, Guo-Liang

APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MB10036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-170

Query Match      8.4%; Score 17; DB 15; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAEIRDP 118
      |||||
Db      22 GVRRRPWGKFAAEIRDP 38

RESULT 14
US-10-374-780A-332
; Sequence 332, Application US/10374780A
; Publication No. US2004001927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J.
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Dubell, Arnold T.
; APPLICANT: Pineda, Omalra
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MB1-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
```

```

; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 332
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1792 (conserved domain in aa coordinates: 17-85)
US-10-374-780A-332

```

```

Query Match      8.4%; Score 17; DB 15; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      102 GVRRRPWGKFAAEIRDP 118
Db      22 GVRRRPWGKFAAEIRDP 38

```

## RESULT 15

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US-10-425-114-41831
; Sequence 41831, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41831
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB25-065-D10_FLI.pep
US-10-425-114-41831

```

```

Query Match      8.4%; Score 17; DB 15; Length 152;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      102 GVRRRPWGKFAAEIRDP 118
Db      60 GVRRRPWGKFAAEIRDP 76

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Search completed: February 27, 2005, 22:38:55
Job time : 130 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2005, 22:17:56 ; Search time 40 Seconds

(without alignments)  
488.300 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 203  
Sequence: 1 MEEETISVDRFLSLIEH.....SSSSSSSSSENSGCRKKRY 203

Scoring table: Oligo  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	9.4	226	2 T00409	ethylene-responsive
2	17	8.4	207	2 T49897	transcription fact
3	17	8.4	236	2 T02432	ethylene-responsiv
4	16	7.9	277	2 T03927	DNA binding protei
5	14	6.9	268	2 T04787	hypothetical prote
6	13	6.4	225	2 A85196	ERBP-2 protein [I
7	13	6.4	233	2 T02590	DNA binding protei
8	13	6.4	234	2 T07686	transcription fact
9	13	6.4	263	2 T51989	ethylene responsiv
10	13	6.4	266	2 T51988	ethylene responsiv
11	13	6.4	281	2 T52189	ethylene responsiv
12	13	6.4	291	2 T02434	DNA binding protei
13	13	6.4	294	2 C84901	probable AP2 domai
14	13	6.4	300	2 T52020	ethylene responsiv
15	13	6.4	315	2 T47955	hypothetical prote
16	13	6.4	349	2 T41394	hypothetical prote
17	13	6.4	603	2 E71444	probable ERBP-4 -
18	12	5.9	236	2 B84718	hypothetical prote
19	12	5.9	244	2 B86197	hypothetical prote
20	12	5.9	262	2 T40941	hypothetical serin
21	12	5.9	303	2 T04541	hypothetical prote
22	11	5.4	297	2 B84731	hypothetical prote
23	11	5.4	468	2 A55476	protein kinase (EC
24	11	5.4	503	2 S63357	probable membrane
25	11	5.4	591	2 T19746	hypothetical prote
26	11	5.4	1341	2 S50366	probable membrane
27	11	5.4	1788	2 T31095	vitellogenin precu
28	11	5.4	1858	2 T18273	1-phosphatidylinos
29	11	5.4	1912	2 T29088	vitellinogenin I pre

30	10	4.9	135	2 T09876	dehydrin - upland
31	10	4.9	145	2 S04042	embryonic abundant
32	10	4.9	149	2 T23179	hypothetical prote
33	10	4.9	153	2 S67294	hypothetical prote
34	10	4.9	164	2 T16168	hypothetical prote
35	10	4.9	166	2 T07089	dehydrin - soybean
36	10	4.9	198	2 A49243	GLOF-C4 protein -
37	10	4.9	216	2 B96794	unknown protein F1
38	10	4.9	228	2 S19132	rab25 protein - ri
39	10	4.9	229	2 UC7219	nuclear protein SR
40	10	4.9	238	2 T52505	hypothetical prote
41	10	4.9	238	2 T32889	hypothetical prote
42	10	4.9	282	2 T21222	hypothetical prote
43	10	4.9	286	2 C61615	sericin MG-2 - gre
44	10	4.9	290	2 T21868	hypothetical prote
45	10	4.9	292	2 I51171	transcription fact

#### ALIGNMENTS

RESULT 1  
T00409  
ethylene-responsive transcription factor homolog T13E15.15 - Arabidopsis thaliana  
N/Alternate names: hypothetical protein At2g44840  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004  
A/Accession: T00409; D84883  
R/Rounsailey, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mas  
submitted to the EMBL Data Library, July 1997  
A/Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.  
A/Reference number: Z14146  
A/Accession: T00409  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-226 <ROU>  
A/Cross-references: UNIPROT:Q22167; EMBL:AC002388; NID:G3420042; PID:G2344900  
A/Experimental source: cultivar Columbia  
R/Lin, X.; Kaul, S.; Rounsailey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Motilal, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
eues, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MIMD:20083487; PMID:10617197  
A/Accession: D84883  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-226 <STO>  
A/Cross-references: GB:AE002093; NID:G2344900; PID:NAC31840.1; GSPDB:GN00139  
A/Gene: At2g44840; T13E15.15  
A/Map position: 2

Query Match 9.4% Score 19; DB 2; Length 226;  
Best Local Similarity 100.0%; Pred No. 1.4e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVARRPWGFPAEIRDPK 120  
Db 94 GVARRPWGFPAEIRDPK 112

RESULT 2  
T49897  
transcription factor-like protein - Arabidopsis thaliana  
N/Alternate names: protein T211.290  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
A/Accession: T49897  
R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; L  
submitted to the Protein Sequence Database, April 2000  
A/Reference number: Z24493  
A/Accession: T49897

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-207 <BEV>  
A:Cross-references: UNIPROT:Q9LY05; EMBL:AL163912; GSPDB:GN00063; ATSP:T211.290  
A:Experimental source: cultivar Columbia; BAC clone T211  
C:Genetics:  
A:Gene: ATSP:T211.290  
A:Map position: 5

Query Match 8.4%; Score 17; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
|||  
Db 112 GVRRRPWGKFAAEIRDP 128

## RESULT 3

T02432  
ethylene-responsive transcription factor ERF1 - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T02432  
R:Ohme-Takagi, M.; Shinshi, H.  
Plant Cell 7, 173-182, 1995  
A:Title: Ethylene-inducible DNA binding proteins that interact with an ethylene response  
A:Reference number: Z14671; MUID:95276459; PMID:7756828  
A:Accession: T02432  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <OHM>  
A:Cross-references: UNIPROT:Q0476; EMBL:D38123; NID:9790359; PID:BA07321.1; PID:g1208  
A:Experimental source: strain BY4; tissue-type leaf

Query Match 8.4%; Score 17; DB 2; Length 236;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
|||  
Db 107 GVRRRPWGKFAAEIRDP 123

## RESULT 4

T03927  
DNA binding protein S25-XP1 - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T03927  
R:Xu, P.; Ling, J.; Li, D.; Hasegawa, P.M.; Bressan, R.A.  
submitted to the EMBL Data Library, December 1996  
A:Reference number: Z15139  
A:Accession: T03927  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <XUP>  
A:Cross-references: UNIPROT:P93392; EMBL:U81157; NID:g1732405; PID:AA38748.1; PID:g173  
A:Experimental source: strain Wisconsin-38

Query Match 7.9%; Score 16; DB 2; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 117  
|||  
Db 94 GVRRRPWGKFAAEIRDP 109

RESULT 5  
T04787  
hypothetical protein F10M10.180 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04787  
R:Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hobeisel, J.; Mewes, H.W.; Mayer,  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15384  
A:Accession: T04787  
A:Molecule type: DNA  
A:Residues: 1-268 <BEV>  
A:Cross-references: UNIPROT:Q9S206; EMBL:AL035521  
A:Experimental source: cultivar Columbia; BAC clone F10M10  
C:Genetics:  
A:Map position: 4  
A:Note: F10M10.180

Query Match 6.9%; Score 14; DB 2; Length 268;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPWGKFAAEIRDP 119  
|||  
Db 142 RPWGKFAAEIRDP 155

## RESULT 6

A85196  
ERBP-2 protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: A85196  
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198  
A:Accession: A85196  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-225 <STO>  
A:Cross-references: GB:NC\_001268; NID:g5281024; PID:CA845963.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: d14785w  
A:Map position: 4

Query Match 6.4%; Score 13; DB 2; Length 225;  
Best Local Similarity 100.0%; Pred. No. 9.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPWGKFAAEIRDP 118  
|||  
Db 111 RPWGKFAAEIRDP 123

## RESULT 7

T02590  
DNA binding protein ERBP-2 - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T02590  
R:Ohme-Takagi, M.; Shinshi, H.  
Plant Cell 7, 173-182, 1995  
A:Title: Ethylene-inducible DNA binding proteins that interact with an ethylene response  
A:Reference number: Z14671; MUID:95276459; PMID:7756828  
A:Accession: T02590  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-233 <OHM>  
A:Cross-references: UNIPROT:Q0479; EMBL:D38126; NID:9790362; PID:BA07324.1; PID:g1208  
A:Experimental source: strain BY4; tissue-type leaf

Query Match 6.4%; Score 13; DB 2; Length 233;  
Best Local Similarity 100.0%; Pred. No. 9.5e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPWGKFAAEIRDP 118

Db 105 RPKGKFAAEIRDP 117

## RESULT 8

T07686  
transcription factor Pt14 - tomato (fragment)  
C/Species: Lycopersicon esculentum (tomato)  
C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C/Accession: T07686  
R/Zhou, Y.; Tang, X.; Martin, G.B.  
submitted to the EMBL Data Library, July 1998  
A/Reference number: Z16094  
A/Accession: T07686  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-234 <ZHO>  
A/Cross-references: UNIPROT:Q04680; EMBL:U89255; NID:g3342210; PIDN:MAC50047.1; PID:g334  
C/Function:  
A/Description: transcription factor  
A/Note: binds the GCC box, present in the promoter region of genes encoding pathogenesis  
C/Keywords: DNA binding; transcription factor

Query Match 6.4%; Score 13; DB 2; Length 214;  
Best Local Similarity 100.0%; Pred. No. 9.9e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 112 RPKGKFAAEIRDP 124

## RESULT 9

T51989  
ethylene responsive element binding factor 2 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C/Accession: T51989  
R/Fujimoto, S.Y.; Ohta, M.; Ueui, A.; Shinshi, H.; Ohme-Takagi, M.  
Plant Cell 12, 393-404, 2000  
A/Title: Arabidopsis ethylene responsive element binding factors act as transcriptional  
A/Reference number: Z25893  
A/Accession: T51989  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-243 <FUJ>  
A/Cross-references: UNIPROT:O80338; EMBL:AB008104; PIDN:BA32419.1  
C/Genetics:  
A/Gene: ERF-2

Query Match 6.4%; Score 13; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 9.9e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 123 RPKGKFAAEIRDP 135

## RESULT 10

T51988  
ethylene responsive element binding factor 1 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 20-Oct-2000  
C/Accession: T51988  
R/Fujimoto, S.Y.; Ohta, M.; Ueui, A.; Shinshi, H.; Ohme-Takagi, M.  
Plant Cell 12, 393-404, 2000  
A/Title: Arabidopsis ethylene responsive element binding factors act as transcriptional  
A/Reference number: Z25893  
A/Accession: T51988  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-266 <FUJ>

A/Cross-references: EMBL:AB008103; PIDN:BA32418.1  
C/Genetics:  
A/Gene: ERF-1

Query Match 6.4%; Score 13; DB 2; Length 266;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 152 RPKGKFAAEIRDP 164

## RESULT 11

T52189  
ethylene responsive element binding factor [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C/Accession: T52189  
R/Ueui, A.; Ohta, M.; Shinshi, H.; Ohme-Takagi, M.  
submitted to the EMBL Data Library, April 1998  
A/Description: Arabidopsis ethylene responsive element binding factor (AtERF5).  
A/Reference number: Z25994  
A/Accession: T52189  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-281 <USU>  
A/Cross-references: UNIPROT:O80387; EMBL:AB013301; PIDN:BA31525.1  
C/Genetics:  
A/Gene: ERF6

Query Match 6.4%; Score 13; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 143 RPKGKFAAEIRDP 155

## RESULT 12

T02434  
DNA binding protein ERFBP-4 - common tobacco  
C/Species: Nicotiana tabacum (common tobacco)  
C/Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C/Accession: T02434  
R/Ohme-Takagi, M.; Shinshi, H.  
Plant Cell 7, 173-182, 1995  
A/Title: Ethylene-inducible DNA binding proteins that interact with an ethylene respons  
A/Reference number: Z14671; MUID:95276459; PMID:7756828  
A/Accession: T02434  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-291 <OHM>  
A/Cross-references: UNIPROT:Q40478; EMBL:J38125; NID:g790361; PIDN:BA07323.1; PID:g120  
A/Experimental source: strain B74; tissue-type leaf  
C/Superfamily: Arabidopsis thaliana hypothetical protein T19P19.170

Query Match 6.4%; Score 13; DB 2; Length 291;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 151 RPKGKFAAEIRDP 163

## RESULT 13

C84901  
probable AP2 domain transcription factor [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: C84901

R./lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentle, M.I.; Town, C.D.; Fujii, C.Y.;  
M. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A./Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A./Reference number: AB4420; MUID:20083487; PMID:10617197

A./Accession: C84901  
A./Status: Preliminary  
A./Molecule type: DNA  
A./Residues: 1294 <STO>  
A./Cross-references: UNIPROT:O82339; GB:AE002093; NID:93702318; PIDN:MAC62875.1; GSPDB:GN  
C./Gene: AC2946310  
A./Map position: 2  
C./Superfamily: *Arabidopsis thaliana* hypothetical protein F15G16.20

Query Match 6.4%; Score 13; DB 2; Length 294;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAEIRDP 118  
DB 105 RFWGKFAEIRDP 117

## RESULT 14

T52020  
ethylene responsive element binding factor 5 [validated] - *Arabidopsis thaliana*

C./Species: *Arabidopsis thaliana* (mouse-ear cress)

C./Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004

C./Accession: T52020

R./Fujimoto, S.Y.; Ohta, M.; Usui, A.; Shinsui, H.; Ohme-Takagi, M.  
Plant Cell 12, 393-404, 2000

A./Title: *Arabidopsis* ethylene responsive element binding factors act as transcriptional

A./Reference number: Z25893

A./Accession: T52020

A./Status: Preliminary; translated from GB/EMBL/DBJ

A./Molecule type: mRNA

A./Residues: 1-300 <PUT>

A./Cross-references: UNIPROT:O80341; EMBL:AB008107; PIDN:BAJ32422.1

C./Gene: ACERF-5

C./Function:

A./Description: acts as a transcriptional activator for GCC box-dependent transcription

Query Match 6.4%; Score 13; DB 2; Length 300;  
Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAEIRDP 118  
DB 162 RFWGKFAEIRDP 174

## RESULT 15

T47955

hypothetical protein F15G16.20 - *Arabidopsis thaliana*

C./Species: *Arabidopsis thaliana* (mouse-ear cress)

C./Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C./Accession: T47955

R./De Haan, M.; Maarse, A.C.; Givelli, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet  
submitted to the Protein Sequence Database, January 2000

A./Reference number: Z24480

A./Accession: T47955

A./Status: Preliminary

A./Molecule type: DNA

A./Residues: 1-315 <DEH>

A./Cross-references: UNIPROT:Q9W374; EMBL:AL132959

A./Experimental source: cultivar Columbia; BAC clone F15G16

C./Gene:

A./Map position: 3

A./Note: F15G16.20

C./Superfamily: *Arabidopsis thaliana* hypothetical protein F15G16.20

Query Match 6.4%; Score 13; DB 2; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAEIRDP 118  
DB 111 RFWGKFAEIRDP 123

Search completed: February 27, 2005, 22:27:10  
Job time : 41 secs